



SEQUENCE LISTING

<110> Sleeman, Matthew
Murison, Greg

<120> Fibroblast Growth Factor Receptors and Methods for Their Use

<130> 11000.1037c5

<150> U.S. 09/823,038

<151> 2001-03-28

<150> U.S. 09/383,586

<151> 1999-08-26

<150> U.S. 09/276,268

<151> 1999-03-25

<150> PCT/NZ00/00015

<151> 2000-02-18

<150> U.S. 60/221,216

<151> 2000-07-25

<150> U.S. 10/157,444

<151> 2000-05-28

<150> PCT/NZ03/00105

<151> 2003-05-27

<160> 145

<170> FastSEQ for Windows Version 4.0

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<211> 384

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<213> Mouse

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tgtgggtggc	cagaagtttg	tgggtgtg	cacgggtgat	gtgtgggtcac	ggcctgatgg	180
ctcctacctc	aacaagctgc	tcatctctcg	ggcccggccag	gatgatgctg	gcatgtacat	240
ctgcctaggt	gcaaatacca	tgggctacag	tttccgtagc	gccttcctca	ctgtattacc	300
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<211> 1967

<212> DNA

<213> Mouse

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ggtagecgcc	ccccgcccag	gccggggccc	ggggcgcggg	gggcgggatg	cggcgcccgg	180
ggcagcgatg	accgcgtcgc	gctgctcagg	ggcccggtc	tgaccccggt	gcctgctgcg	240
cgcccccgcg	ctgatccctg	tcgagcgtct	acgcgcctcg	cttcctttgc	ctggagctcg	300
gcgccgaggg	gggcgggacc	ctggctctgc	ggccgcgacc	tgggtcttgc	gggcctgagc	360
cctgagtggc	gtccagtcca	gctcccagtg	accgcgcccc	tgcttcagg	ccgaccggcg	420
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cggcgcgaga	tgatattagt	ccagggaagg	agagccctgg	gccagtggtg	tcttcggggg	540
gccaggagga	cccagccagc	cagcagtggg	cacggcctcg	cttcacacag	ccctccaaga	600
tgaggcgccg	agtgattgca	cggcctgtgg	gtagctctgt	gcggctcaag	tgtgtggcca	660
gtgggcaccc	acggccagac	atcatgtgga	tgaaggatga	ccagaccttg	acgcatctag	720
aggctagtga	acacagaaa	aagaagtgga	cactgagctt	gaagaacctg	aagcctgaag	780

Gly	Arg	His	Asn	Ser	Thr	Ile	Asp	Val	Gly	Gly	Gln	Lys	Phe	Val	Val
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Leu	Pro	Thr	Gly	Asp	Val	Trp	Ser	Arg	Pro	Asp	Gly	Ser	Tyr	Leu	Asn
	50					55					60				
Lys	Leu	Leu	Ile	Ser	Arg	Ala	Arg	Gln	Asp	Asp	Ala	Gly	Met	Tyr	Ile
65					70					75					80
Cys	Leu	Gly	Ala	Asn	Thr	Met	Gly	Tyr	Ser	Phe	Arg	Ser	Ala	Phe	Leu
				85					90					95	
Thr	Val	Leu	Pro	Asp	Pro	Lys	Pro	Pro	Gly	Pro	Pro	Met	Ala	Ser	Ser
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Ser	Ser	Ser	Thr	Ser	Leu	Pro	Trp	Pro	Val	Xaa	Gly	Ile	Pro		
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<210> 6

<211> 529

<212> PRT

<213> Mouse

<400> 6

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Pro	Arg	Gln	Val	Ala	Arg	Leu	Gly	Arg	Thr	Val	Arg	Leu	Gln	Cys	Pro
		35					40					45			
Val	Glu	Gly	Asp	Pro	Pro	Pro	Leu	Thr	Met	Trp	Thr	Lys	Asp	Gly	Arg
	50					55					60				
Thr	Ile	His	Ser	Gly	Trp	Ser	Arg	Phe	Arg	Val	Leu	Pro	Gln	Gly	Leu
65					70					75					80
Lys	Val	Lys	Glu	Val	Glu	Ala	Glu	Asp	Ala	Gly	Val	Tyr	Val	Cys	Lys
				85					90					95	
Ala	Thr	Asn	Gly	Phe	Gly	Ser	Leu	Ser	Val	Asn	Tyr	Thr	Leu	Ile	Ile
			100					105					110		
Met	Asp	Asp	Ile	Ser	Pro	Gly	Lys	Glu	Ser	Pro	Gly	Pro	Gly	Gly	Ser
	115					120						125			
Ser	Gly	Gly	Gln	Glu	Asp	Pro	Ala	Ser	Gln	Gln	Trp	Ala	Arg	Pro	Arg
	130					135					140				
Phe	Thr	Gln	Pro	Ser	Lys	Met	Arg	Arg	Arg	Val	Ile	Ala	Arg	Pro	Val
145					150					155					160
Gly	Ser	Ser	Val	Arg	Leu	Lys	Cys	Val	Ala	Ser	Gly	His	Pro	Arg	Pro
				165					170					175	
Asp	Ile	Met	Trp	Met	Lys	Asp	Asp	Gln	Thr	Leu	Thr	His	Leu	Glu	Ala
			180					185					190		
Ser	Glu	His	Arg	Lys	Lys	Lys	Trp	Thr	Leu	Ser	Leu	Lys	Asn	Leu	Lys
		195					200					205			
Pro	Glu	Asp	Ser	Gly	Lys	Tyr	Thr	Cys	Arg	Val	Ser	Asn	Lys	Ala	Gly
	210					215						220			
Ala	Ile	Asn	Ala	Thr	Tyr	Lys	Val	Asp	Val	Ile	Gln	Arg	Thr	Arg	Ser
225					230					235					240
Lys	Pro	Val	Leu	Thr	Gly	Thr	His	Pro	Val	Asn	Thr	Thr	Val	Asp	Phe
				245					250					255	
Gly	Gly	Thr	Thr	Ser	Phe	Gln	Cys	Lys	Val	Arg	Ser	Asp	Val	Lys	Pro
		260						265					270		
Val	Ile	Gln	Trp	Leu	Lys	Arg	Val	Glu	Tyr	Gly	Ser	Glu	Gly	Arg	His
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Asn	Ser	Thr	Ile	Asp	Val	Gly	Gln	Lys	Phe	Val	Val	Leu	Pro	Thr	
		290				295					300				

Gly Asp Val Trp Ser Arg Pro Asp Gly Ser Tyr Leu Asn Lys Leu Leu
 305 310 315 320
 Ile Ser Arg Ala Arg Gln Asp Asp Ala Gly Met Tyr Ile Cys Leu Gly
 325 330 335
 Ala Asn Thr Met Gly Tyr Ser Phe Arg Ser Ala Phe Leu Thr Val Leu
 340 345 350
 Pro Asp Pro Lys Pro Pro Gly Pro Pro Met Ala Ser Ser Ser Ser
 355 360 365
 Thr Ser Leu Pro Trp Pro Val Val Ile Gly Ile Pro Ala Gly Ala Val
 370 375 380
 Phe Ile Leu Gly Thr Val Leu Leu Trp Leu Cys Gln Thr Lys Lys Lys
 385 390 395 400
 Pro Cys Ala Pro Ala Ser Thr Leu Pro Val Pro Gly His Arg Pro Pro
 405 410 415
 Gly Thr Ser Arg Glu Arg Ser Gly Asp Lys Asp Leu Pro Ser Leu Ala
 420 425 430
 Val Gly Ile Cys Glu Glu His Gly Ser Ala Met Ala Pro Gln His Ile
 435 440 445
 Leu Ala Ser Gly Ser Thr Ala Gly Pro Lys Leu Tyr Pro Lys Leu Tyr
 450 455 460
 Thr Asp Val His Thr His Thr His Thr His Thr Cys Thr His Thr Leu
 465 470 475 480
 Ser Cys Gly Gly Gln Gly Ser Ser Thr Pro Ala Cys Pro Leu Ser Val
 485 490 495
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 35 40 45
 Trp Ala Arg Pro Arg Phe Thr Gln Pro Ser Lys Met Arg Arg Arg Val
 50 55 60
 Ile Ala Arg Pro Val Gly Ser Ser Val Arg Leu Lys Cys Val Ala Ser
 65 70 75 80
 Gly His Pro Arg Pro Asp Ile Met Trp Met Lys Asp Asp Gln Thr Leu
 85 90 95
 Thr His Leu Glu Ala Ser Glu His Arg Lys Lys Lys Trp Thr Leu Ser
 100 105 110
 Leu Lys Asn Leu Lys Pro Glu Asp Ser Gly Lys Tyr Thr Cys Arg Val
 115 120 125
 Ser Asn Lys Ala Gly Ala Ile Asn Ala Thr Tyr Lys Val Asp Val Ile
 130 135 140
 Gln Arg Thr Arg Ser Lys Pro Val Leu Thr Gly Thr His Pro Val Asn
 145 150 155 160

Thr	Thr	Val	Asp	Phe	Gly	Gly	Thr	Thr	Ser	Phe	Gln	Cys	Lys	Val	Arg	
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Ser	Asp	Val	Lys	Pro	Val	Ile	Gln	Trp	Leu	Lys	Arg	Val	Glu	Tyr	Gly	
			180					185					190			
Ser	Glu	Gly	Arg	His	Asn	Ser	Thr	Ile	Asp	Val	Gly	Gly	Gln	Lys	Phe	
		195					200					205				
Val	Val	Leu	Pro	Thr	Gly	Asp	Val	Trp	Ser	Arg	Pro	Asp	Gly	Ser	Tyr	
	210					215					220					
Leu	Asn	Lys	Leu	Leu	Ile	Ser	Arg	Ala	Arg	Gln	Asp	Asp	Ala	Gly	Met	
225					230					235					240	
Tyr	Ile	Cys	Leu	Gly	Ala	Asn	Thr	Met	Gly	Tyr	Ser	Phe	Arg	Ser	Ala	
				245					250						255	
Phe	Leu	Thr	Val	Leu	Pro	Asp	Pro	Lys	Pro	Pro	Pro	Gly	Pro	Pro	Met	
			260					265					270			
Ala	Ser	Ser	Ser	Ser	Ser	Thr	Ser	Leu	Pro	Trp	Pro	Val	Val	Ile	Gly	
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Ile	Pro	Ala	Gly	Ala	Val	Phe	Ile	Leu	Gly	Thr	Val	Leu	Leu	Trp	Leu	
	290					295					300					
Cys	Gln	Thr	Lys	Lys	Lys	Pro	Cys	Ala	Pro	Ala	Ser	Thr	Leu	Pro	Val	
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Pro	Gly	His	Arg	Pro	Pro	Gly	Thr	Ser	Arg	Glu	Arg	Ser	Gly	Asp	Lys	
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Asp	Leu	Pro	Ser	Leu	Ala	Val	Gly	Ile	Cys	Glu	Glu	His	Gly	Ser	Ala	
			340					345					350			
Met	Ala	Pro	Gln	His	Ile	Leu	Ala	Ser	Gly	Ser	Thr	Ala	Gly	Pro	Lys	
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	370					375					380					
Thr	Cys	Thr	His	Thr	Leu	Ser	Cys	Gly	Gly	Gln	Gly	Ser	Ser	Thr	Pro	
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Ala	Cys	Pro	Leu	Ser	Val	Leu	Asn	Thr	Ala	Asn	Leu	Gln	Ala	Leu	Cys	
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Pro	Glu	Val	Gly	Ile	Trp	Gly	Pro	Arg	Gln	Gln	Val	Gly	Arg	Ile	Glu	
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Asn	Asn	Gly	Gly	Arg	Val	Ser										
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 35 40 45
 Val Pro Val Glu Gly Asp Pro Pro Pro Leu Thr Met Trp Thr Lys Asp
 50 55 60
 Gly Arg Thr Ile His Ser Gly Trp Ser Arg Phe Arg Val Leu Pro Gln
 65 70 75 80
 Gly Leu Lys Val Lys Gln Val Glu Arg Glu Asp Ala Gly Val Tyr Val
 85 90 95
 Cys Lys Ala Thr Asn Gly Phe Gly Ser Leu Ser Val Asn Tyr Thr Leu
 100 105 110

Val	Val	Leu	Asp	Asp	Ile	Ser	Pro	Gly	Lys	Glu	Ser	Leu	Gly	Pro	Asp
		115					120					125			
Ser	Ser	Ser	Gly	Gly	Gln	Glu	Asp	Pro	Ala	Ser	Gln	Gln	Trp	Ala	Arg
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Pro	Arg	Phe	Thr	Gln	Pro	Ser	Lys	Met	Arg	Arg	Val	Ile	Ala	Arg	
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Arg	Pro	Asp	Ile	Thr	Trp	Met	Lys	Asp	Asp	Gln	Ala	Leu	Thr	Arg	Pro
			180					185					190		
Glu	Ala	Ala	Glu	Pro	Arg	Lys	Lys	Lys	Trp	Thr	Leu	Ser	Leu	Lys	Asn
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Ala	Gly	Ala	Ile	Asn	Ala	Thr	Tyr	Lys	Val	Asp	Val	Ile	Gln	Arg	Thr
225					230					235				240	
Arg	Ser	Lys	Pro	Val	Leu	Thr	Gly	Thr	His	Pro	Val	Asn	Thr	Thr	Val
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Asp	Phe	Gly	Gly	Thr	Thr	Ser	Phe	Gln	Cys	Lys	Val	Arg	Ser	Asp	Val
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Lys	Pro	Val	Ile	Gln	Trp	Leu	Lys	Arg	Val	Glu	Tyr	Gly	Ala	Glu	Gly
		275					280					285			
Arg	His	Asn	Ser	Thr	Ile	Asp	Val	Gly	Gly	Gln	Lys	Phe	Val	Val	Leu
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<210> 13
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Pro Arg Gln Val Ala Arg Leu Gly Arg Thr Val Arg Leu Gln Cys Pro
35 40 45
Val Glu Gly Asp Pro Pro Pro Leu Thr Met Trp Thr Lys Asp Gly Arg
50 55 60
Thr Ile His Ser Gly Trp Ser Arg Phe Arg Val Leu Pro Gln Gly Leu
65 70 75 80
Lys Val Lys Glu Val Glu Ala Glu Asp Ala Gly Val Tyr Val Cys Lys
85 90 95
Ala Thr Asn Gly Phe Gly Ser Leu Ser Val Asn Tyr Thr Leu Ile Ile
100 105 110
Met Asp Asp Ile Ser Pro Gly Lys Glu Ser Pro Gly Pro Gly Gly Ser
115 120 125
Ser Gly Gly Gln Glu Asp Pro Ala Ser Gln Gln Trp Ala Arg Pro Arg
130 135 140
Phe Thr Gln Pro Ser Lys Met Arg Arg Arg Val Ile Ala Arg Pro Val
145 150 155 160
Gly Ser Ser Val Arg Leu Lys Cys Val Ala Ser Gly His Pro Arg Pro
165 170 175
Asp Ile Met Trp Met Lys Asp Asp Gln Thr Leu Thr His Leu Glu Ala
180 185 190
Ser Glu His Arg Lys Lys Lys Trp Thr Leu Ser Leu Lys Asn Leu Lys

195	200	205
Pro Glu Asp Ser Gly Lys Tyr Thr Cys Arg Val Ser Asn Lys Ala Gly		
210	215	220
Ala Ile Asn Ala Thr Tyr Lys Val Asp Val Ile Gln Arg Thr Arg Ser		
225	230	235
Lys Pro Val Leu Thr Gly Thr His Pro Val Asn Thr Thr Val Asp Phe		
245	250	255
Gly Gly Thr Thr Ser Phe Gln Cys Lys Val Arg Ser Asp Val Lys Pro		
260	265	270
Val Ile Gln Trp Leu Lys Arg Val Glu Tyr Gly Ser Glu Gly Arg His		
275	280	285
Asn Ser Thr Ile Asp Val Gly Gly Gln Lys Phe Val Val Leu Pro Thr		
290	295	300
Gly Asp Val Trp Ser Arg Pro Asp Gly Ser Tyr Leu Asn Lys Leu Leu		
305	310	315
Ile Ser Arg Ala Arg Gln Asp Asp Ala Gly Met Tyr Ile Cys Leu Gly		
325	330	335
Ala Asn Thr Met Gly Tyr Ser Phe Arg Ser Ala Phe Leu Thr Val Leu		
340	345	350
Pro Asp Pro Lys Pro Pro Gly Pro Pro Met Ala Ser Ser Ser Ser Ser		
355	360	365
Thr Ser Leu Pro Trp		
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<210> 14
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Asp Leu Pro Ser Leu Ala Val Gly Ile Cys Glu Glu His Gly Ser Ala
35 40 45
Met Ala Pro Gln His Ile Leu Ala Ser Gly Ser Thr Ala Gly Pro Lys
50 55 60
Leu Tyr Pro Lys Leu Tyr Thr Asp Val His Thr His Thr His
65 70 75 80
Thr Cys Thr His Thr Leu Ser Cys Gly Gly Gln Gly Ser Ser Thr Pro
85 90 95
Ala Cys Pro Leu Ser Val Leu Asn Thr Ala Asn Leu Gln Ala Leu Cys
100 105 110
Pro Glu Val Gly Ile Trp Gly Pro Arg Gln Gln Val Gly Arg Ile Glu
115 120 125
Asn Asn Gly Gly Arg Val Ser
130 135

<210> 15
 <211> 37
 <212> PRT
 <213> Mouse

<400> 15

Arg Val Glu Tyr Gly Ser Glu Gly Arg His Asn Ser Thr Ile Asp Val

1	5	10	15
Gly Gly Gln Lys Phe Val Val Leu Pro Thr Gly Asp Val Trp Ser Arg			
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Pro Asp Gly Ser Tyr			
35			

<210> 16
 <211> 1515
 <212> DNA
 <213> Human

<400> 16

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gcccggctgg	gccgcactgt	gcggctgcag	tgcccagtgg	agggggaccc	gccgccgctg	180
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ccgcaggggc	tgaaggtgaa	gcaggtggag	cgggaggatg	ccggcgtgta	cgtgtgcaag	300
gccaccaacg	gcttcggcag	ccttagcgct	aactacaccc	tcgtcgtgct	ggatgacatt	360
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gacatcacgt	ggatgaagga	cgaccaggcc	ttgacgcgcc	cagaggccgc	tgagcccagg	600
aagaagaagt	ggacactgag	cctgaagaac	ctgcggcccg	aggacagcgg	caaatacacc	660
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ccgcaagggc	cacctgtggc	ctcctcgtcc	tcggccacta	gcctgccgtg	gcccgtgggc	1140
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ggcccaggcc	cagttgctgg	ccctaagttg	taccccaaac	tctacacaga	catccacaca	1440
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<210> 17
 <211> 504
 <212> PRT
 <213> Human

<400> 17

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Gly Ala Phe Pro Pro Ala Ala Ala Ala Arg Gly Pro Pro Lys Met Ala	
	20
Asp Lys Val Val Pro Arg Gln Val Ala Arg Leu Gly Arg Thr Val Arg	
	35
Leu Gln Cys Pro Val Glu Gly Asp Pro Pro Pro Leu Thr Met Trp Thr	
	50
Lys Asp Gly Arg Thr Ile His Ser Gly Trp Ser Arg Phe Arg Val Leu	
	65
Pro Gln Gly Leu Lys Val Lys Gln Val Glu Arg Glu Asp Ala Gly Val	
	85
	90
	95

Tyr	Val	Cys	Lys	Ala	Thr	Asn	Gly	Phe	Gly	Ser	Leu	Ser	Val	Asn	Tyr	100	105	110
Thr	Leu	Val	Val	Leu	Asp	Asp	Ile	Ser	Pro	Gly	Lys	Glu	Ser	Leu	Gly	115	120	125
Pro	Asp	Ser	Ser	Ser	Gly	Gly	Gln	Glu	Asp	Pro	Ala	Ser	Gln	Gln	Trp	130	135	140
Ala	Arg	Pro	Arg	Phe	Thr	Gln	Pro	Ser	Lys	Met	Arg	Arg	Arg	Val	Ile	145	150	155
Ala	Arg	Pro	Val	Gly	Ser	Ser	Val	Arg	Leu	Lys	Cys	Val	Ala	Ser	Gly	165	170	175
His	Pro	Arg	Pro	Asp	Ile	Thr	Trp	Met	Lys	Asp	Asp	Gln	Ala	Leu	Thr	180	185	190
Arg	Pro	Glu	Ala	Ala	Glu	Pro	Arg	Lys	Lys	Lys	Trp	Thr	Leu	Ser	Leu	195	200	205
Lys	Asn	Leu	Arg	Pro	Glu	Asp	Ser	Gly	Lys	Tyr	Thr	Cys	Arg	Val	Ser	210	215	220
Asn	Arg	Ala	Gly	Ala	Ile	Asn	Ala	Thr	Tyr	Lys	Val	Asp	Val	Ile	Gln	225	230	235
Arg	Thr	Arg	Ser	Lys	Pro	Val	Leu	Thr	Gly	Thr	His	Pro	Val	Asn	Thr	245	250	255
Thr	Val	Asp	Phe	Gly	Gly	Thr	Thr	Ser	Phe	Gln	Cys	Lys	Val	Arg	Ser	260	265	270
Asp	Val	Lys	Pro	Val	Ile	Gln	Trp	Leu	Lys	Arg	Val	Glu	Tyr	Gly	Ala	275	280	285
Glu	Gly	Arg	His	Asn	Ser	Thr	Ile	Asp	Val	Gly	Gly	Gln	Lys	Phe	Val	290	295	300
Val	Leu	Pro	Thr	Gly	Asp	Val	Trp	Ser	Arg	Pro	Asp	Gly	Ser	Tyr	Leu	305	310	315
Asn	Lys	Leu	Leu	Ile	Thr	Arg	Ala	Arg	Gln	Asp	Asp	Ala	Gly	Met	Tyr	325	330	335
Ile	Cys	Leu	Gly	Ala	Asn	Thr	Met	Gly	Tyr	Ser	Phe	Arg	Ser	Ala	Phe	340	345	350
Leu	Thr	Val	Leu	Pro	Asp	Pro	Lys	Pro	Gln	Gly	Pro	Pro	Val	Ala	Ser	355	360	365
Ser	Ser	Ser	Ala	Thr	Ser	Leu	Pro	Trp	Pro	Val	Val	Ile	Gly	Ile	Pro	370	375	380
Ala	Gly	Ala	Val	Phe	Ile	Leu	Gly	Thr	Leu	Leu	Leu	Trp	Leu	Cys	Gln	385	390	395
Ala	Gln	Lys	Lys	Pro	Cys	Thr	Pro	Ala	Pro	Ala	Pro	Pro	Leu	Pro	Gly	405	410	415
His	Arg	Pro	Pro	Gly	Thr	Ala	Arg	Asp	Arg	Ser	Gly	Asp	Lys	Asp	Leu	420	425	430
Pro	Ser	Leu	Ala	Ala	Leu	Ser	Ala	Gly	Pro	Gly	Val	Gly	Leu	Cys	Glu	435	440	445
Glu	His	Gly	Ser	Pro	Ala	Ala	Pro	Gln	His	Leu	Leu	Gly	Pro	Gly	Pro	450	455	460
Val	Ala	Gly	Pro	Lys	Leu	Tyr	Pro	Lys	Leu	Tyr	Thr	Asp	Ile	His	Thr	465	470	475
His	Thr	His	Thr	His	Ser	His	Thr	His	Ser	His	Val	Glu	Gly	Lys	Val	485	490	495
His	Gln	His	Ile	His	Tyr	Gln	Cys									500		

<210> 18

<211> 1161

<212> DNA

<213> Human

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<400> 18
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gcccggctgg gccgcactgt gcggtgcag tgcccagtgg agggggaccc gccgcgctg    180
accatgtgga ccaaggatgg ccgcaccatc cacagcggct ggagccgctt ccgctgctg    240
ccgcaggggc tgaaggtgaa gcaggtggag cgggaggatg ccggcgtgta cgtgtgcaag    300
gccaccaacg gcttcggcag ccttagcgtc aactacaccc tcgtcgtgct ggatgacatt    360
agcccaggga aggagagcct ggggcccgcac agctcctctg ggggtcaaga ggaccccgcc    420
agccagcagt gggcacgacc gcgcttcaca cagccctcca agatgaggcg ccgggtgatc    480
gcacggcccc tgggtagctc cgtgcggctc aagtgcgtgg ccagcgggca ccctcggccc    540
gacatcacgt ggatgaagga cgaccaggcc ttgacgcgcc cagagggcgc tgagcccagg    600
aagaagaagt ggacactgag cctgaagaac ctgcggccgg aggcagcgg caaatacacc    660
tgccgcgtgt cgaaccgcgc gggcgccatc aacgccacct acaaggtgga tgtgatccac    720
ccaaaaccgc aagggccacc tgtggcctcc tcgtcctcgg ccactagcct gccgtggccc    780
gtggtcatcg gcatcccagc cggcgctgtc ttcatcctgg gcaccctgct cctgtggctt    840
tgccaggccc agaagaagcc gtgcaccccc gcgcctgccc ctcccctgcc tgggcaccgc    900
ccgcccggga cggcccgcga ccgcagcgga gacaaggacc ttccctcggt ggccgcccctc    960
agcgtggccc ctggtgtggg gctgtgtgag gagcatgggt ctccggcagc cccccagcac   1020
ttactgggcc caggcccagt tgctggccct aagttgtacc ccaaactcta cacagacatc   1080
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cacatccact atcagtgcta g                                     1161

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<210> 19
<211> 386
<212> PRT
<213> Human

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<400> 19
Met Thr Pro Ser Pro Leu Leu Leu Leu Leu Leu Pro Pro Leu Leu Leu
 1              5              10              15

Gly Ala Phe Pro Pro Ala Ala Ala Ala Arg Gly Pro Pro Lys Met Ala
                20                25                30
Asp Lys Val Val Pro Arg Gln Val Ala Arg Leu Gly Arg Thr Val Arg
 35              40              45
Leu Gln Cys Pro Val Glu Gly Asp Pro Pro Pro Leu Thr Met Trp Thr
 50              55              60
Lys Asp Gly Arg Thr Ile His Ser Gly Trp Ser Arg Phe Arg Val Leu
 65              70              75              80
Pro Gln Gly Leu Lys Val Lys Gln Val Glu Arg Glu Asp Ala Gly Val
                85              90              95
Tyr Val Cys Lys Ala Thr Asn Gly Phe Gly Ser Leu Ser Val Asn Tyr
 100             105             110
Thr Leu Val Val Leu Asp Asp Ile Ser Pro Gly Lys Glu Ser Leu Gly
 115             120             125
Pro Asp Ser Ser Ser Gly Gly Gln Glu Asp Pro Ala Ser Gln Gln Trp
 130             135             140
Ala Arg Pro Arg Phe Thr Gln Pro Ser Lys Met Arg Arg Arg Val Ile

145              150              155              160
Ala Arg Pro Val Gly Ser Ser Val Arg Leu Lys Cys Val Ala Ser Gly
                165              170              175
His Pro Arg Pro Asp Ile Thr Trp Met Lys Asp Asp Gln Ala Leu Thr

                180              185              190
Arg Pro Glu Ala Ala Glu Pro Arg Lys Lys Lys Trp Thr Leu Ser Leu

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<213> Human

<400> 21

Met	Thr	Pro	Ser	Pro	Leu	Leu	Leu	Leu	Leu	Leu	Pro	Pro	Leu	Leu	Leu
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Gly	Ala	Phe	Pro	Pro	Ala	Ala	Ala	Ala	Arg	Gly	Pro	Pro	Lys	Met	Ala
			20					25					30		
Asp	Lys	Val	Val	Pro	Arg	Gln	Val	Ala	Arg	Leu	Gly	Arg	Thr	Val	Arg
		35					40					45			
Leu	Gln	Cys	Pro	Val	Glu	Gly	Asp	Pro	Pro	Pro	Leu	Thr	Met	Trp	Thr
	50					55					60				
Lys	Asp	Gly	Arg	Thr	Ile	His	Ser	Gly	Trp	Ser	Arg	Phe	Arg	Val	Leu
65					70				75					80	
Pro	Gln	Gly	Leu	Lys	Val	Lys	Gln	Val	Glu	Arg	Glu	Asp	Ala	Gly	Val
				85					90					95	
Tyr	Val	Cys	Lys	Ala	Thr	Asn	Gly	Phe	Gly	Ser	Leu	Ser	Val	Asn	Tyr
			100					105					110		
Thr	Leu	Val	Val	Leu	Asp	Asp	Ile	Ser	Pro	Gly	Lys	Glu	Ser	Leu	Gly
		115					120					125			
Pro	Asp	Ser	Ser	Ser	Gly	Gly	Gln	Glu	Asp	Pro	Ala	Ser	Gln	Gln	Trp
	130					135					140				
Glu	Arg	Thr	Arg	Ser	Lys	Pro	Val	Leu	Thr	Gly	Thr	His	Pro	Val	Asn
145					150				155					160	
Thr	Thr	Val	Asp	Phe	Gly	Gly	Thr	Thr	Ser	Phe	Gln	Cys	Lys	Val	Arg
				165					170					175	
Ser	Asp	Val	Lys	Pro	Val	Ile	Gln	Trp	Leu	Lys	Arg	Val	Glu	Tyr	Gly
			180					185					190		
Ala	Glu	Gly	Arg	His	Asn	Ser	Thr	Ile	Asp	Val	Gly	Gly	Gln	Lys	Phe
		195					200					205			
Val	Val	Leu	Pro	Thr	Gly	Asp	Val	Trp	Ser	Arg	Pro	Asp	Gly	Ser	Tyr
	210					215					220				
Leu	Asn	Lys	Leu	Leu	Ile	Thr	Arg	Ala	Arg	Gln	Asp	Asp	Ala	Gly	Met
225					230					235				240	
Tyr	Ile	Cys	Leu	Gly	Ala	Asn	Thr	Met	Gly	Tyr	Ser	Phe	Arg	Ser	Ala
				245					250					255	
Phe	Leu	Thr	Val	Leu	Pro	Asp	Pro	Lys	Pro	Gln	Gly	Pro	Pro	Val	Ala
			260					265					270		
Ser	Ser	Ser	Ser	Ala	Thr	Ser	Leu	Pro	Trp	Pro	Val	Val	Ile	Gly	Ile
			275				280					285			
Pro	Ala	Gly	Ala	Val	Phe	Ile	Leu	Gly	Thr	Leu	Leu	Leu	Trp	Leu	Cys
	290					295					300				
Gln	Ala	Gln	Lys	Lys	Pro	Cys	Thr	Pro	Ala	Pro	Ala	Pro	Pro	Leu	Pro
305					310				315					320	
Gly	His	Arg	Pro	Pro	Gly	Thr	Ala	Arg	Asp	Arg	Ser	Gly	Asp	Lys	Asp
				325					330					335	
Leu	Pro	Ser	Leu	Ala	Ala	Leu	Ser	Ala	Gly	Pro	Gly	Val	Gly	Leu	Cys
			340					345					350		
Glu	Glu	His	Gly	Ser	Pro	Ala	Ala	Pro	Gln	His	Leu	Leu	Gly	Pro	Gly
		355					360					365			
Pro	Val	Ala	Gly	Pro	Lys	Leu	Tyr	Pro	Lys	Leu	Tyr	Thr	Asp	Ile	His
	370					375					380				
Thr	His	Thr	His	Thr	His	Ser	His	Thr	His	Ser	His	Val	Glu	Gly	Lys
385					390					395					400
Val	His	Gln	His	Ile	His	Tyr	Gln	Cys							
				405											

<210> 22

<211> 1434
 <212> DNA
 <213> Human

<400> 22

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gcccggctgg	gccgcaactgt	gcggctgcag	tgcccagtgg	agggggaccc	gccgccgctg	180
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gccaccaacg	gcttcggcag	ccttagcgct	aactacaccc	tcgtcgtgct	ggcacgaccg	360
cgcttcacac	agccctccaa	gatgaggcgc	cgggtgatcg	cacggcccgt	gggtagctcc	420
gtgcggctca	agtgcgtggc	cagcgggcac	cctcggcccc	acatcacgtg	gatgaaggac	480
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ttccgcagcg	ccttcctcac	cgtgctgcc	gacccaaaac	cgcaagggcc	acctgtggcc	1020
tcctcgtcct	cggccactag	cctgcctggt	cccgtgggtc	tcggcatccc	agccggcgct	1080
gtcttcatcc	tgggcaccc	gctcctgtgg	ctttgccagg	cccagaagaa	gccgtgcacc	1140
cccgcgcctg	cccctcccct	gcctgggcac	cgcccgcggg	ggacggcccc	cgaccgcagc	1200
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cctaagtgtg	accccaact	ctacacagac	atccacacac	acacacacac	acactctcac	1380
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<210> 23
 <211> 477
 <212> PRT
 <213> Human

<400> 23

Met	Thr	Pro	Ser	Pro	Leu	Leu	Leu	Leu	Leu	Pro	Pro	Leu	Leu	Leu
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Gly	Ala	Phe	Pro	Pro	Ala	Ala	Ala	Ala	Arg	Gly	Pro	Pro	Lys	Met
			20					25					30	Ala
Asp	Lys	Val	Val	Pro	Arg	Gln	Val	Ala	Arg	Leu	Gly	Arg	Thr	Val
		35					40					45		Arg
Leu	Gln	Cys	Pro	Val	Glu	Gly	Asp	Pro	Pro	Pro	Leu	Thr	Met	Trp
		50				55					60			Thr
Lys	Asp	Gly	Arg	Thr	Ile	His	Ser	Gly	Trp	Ser	Arg	Phe	Arg	Val
65					70				75					80
Pro	Gln	Gly	Leu	Lys	Val	Lys	Gln	Val	Glu	Arg	Glu	Asp	Ala	Gly
				85					90					95
Tyr	Val	Cys	Lys	Ala	Thr	Asn	Gly	Phe	Gly	Ser	Leu	Ser	Val	Asn
			100					105					110	Tyr
Thr	Leu	Val	Val	Leu	Ala	Arg	Pro	Arg	Phe	Thr	Gln	Pro	Ser	Lys
		115					120					125		Met
Arg	Arg	Arg	Val	Ile	Ala	Arg	Pro	Val	Gly	Ser	Ser	Val	Arg	Leu
		130				135					140			Lys
Cys	Val	Ala	Ser	Gly	His	Pro	Arg	Pro	Asp	Ile	Thr	Trp	Met	Lys
145					150				155					160
Asp	Gln	Ala	Leu	Thr	Arg	Pro	Glu	Ala	Ala	Glu	Pro	Arg	Lys	Lys

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ttcctcaccg	tgctgccaga	cccaaaaccg	caagggccac	ctgtggcctc	ctcgtcctcg	840
gccactagcc	tgccgtggcc	cgtggtcac	ggcatcccag	ccggcgctgt	cttcacacctg	900
ggcacctgc	tcctgtggct	ttgccaggcc	cagaagaagc	cgtgcacccc	cgcgctgccc	960
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cttccctcgt	tggccgcctg	cagcgtggc	cctgggtgtgg	ggctgtgtga	ggagcatggg	1080
tctccggcag	ccccccagca	cttactgggc	ccaggcccag	ttgctggccc	taagtgtgac	1140
cccaaactct	acacagacat	ccacacacac	acacacacac	actctcacac	acactcacac	1200
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<210> 25

<211> 413

<212> PRT

<213> Human

<400> 25

Met	Thr	Pro	Ser	Pro	Leu	Leu	Leu	Leu	Leu	Leu	Pro	Pro	Leu	Leu	Leu
1				5						10				15	
Gly	Ala	Phe	Pro	Pro	Ala	Ala	Ala	Ala	Arg	Asp	Asp	Ile	Ser	Pro	Gly
			20					25					30		
Lys	Glu	Ser	Leu	Gly	Pro	Asp	Ser	Ser	Ser	Gly	Gly	Gln	Glu	Asp	Pro
		35					40					45			
Ala	Ser	Gln	Gln	Trp	Ala	Arg	Pro	Arg	Phe	Thr	Gln	Pro	Ser	Lys	Met
		50				55					60				
Arg	Arg	Arg	Val	Ile	Ala	Arg	Pro	Val	Gly	Ser	Ser	Val	Arg	Leu	Lys
65					70					75					80
Cys	Val	Ala	Ser	Gly	His	Pro	Arg	Pro	Asp	Ile	Thr	Trp	Met	Lys	Asp
				85					90					95	
Asp	Gln	Ala	Leu	Thr	Arg	Pro	Glu	Ala	Ala	Glu	Pro	Arg	Lys	Lys	Lys
			100					105					110		
Trp	Thr	Leu	Ser	Leu	Lys	Asn	Leu	Arg	Pro	Glu	Asp	Ser	Gly	Lys	Tyr
		115					120					125			
Thr	Cys	Arg	Val	Ser	Asn	Arg	Ala	Gly	Ala	Ile	Asn	Ala	Thr	Tyr	Lys
	130					135					140				
Val	Asp	Val	Ile	Gln	Arg	Thr	Arg	Ser	Lys	Pro	Val	Leu	Thr	Gly	Thr
145					150					155					160
His	Pro	Val	Asn	Thr	Thr	Val	Asp	Phe	Gly	Gly	Thr	Thr	Ser	Phe	Gln
				165					170					175	
Cys	Lys	Val	Arg	Ser	Asp	Val	Lys	Pro	Val	Ile	Gln	Trp	Leu	Lys	Arg
			180					185					190		
Val	Glu	Tyr	Gly	Ala	Glu	Gly	Arg	His	Asn	Ser	Thr	Ile	Asp	Val	Gly
	195						200					205			
Gly	Gln	Lys	Phe	Val	Val	Leu	Pro	Thr	Gly	Asp	Val	Trp	Ser	Arg	Pro
	210					215					220				
Asp	Gly	Ser	Tyr	Leu	Asn	Lys	Leu	Leu	Ile	Thr	Arg	Ala	Arg	Gln	Asp
225					230					235				240	
Asp	Ala	Gly	Met	Tyr	Ile	Cys	Leu	Gly	Ala	Asn	Thr	Met	Gly	Tyr	Ser
				245					250					255	
Phe	Arg	Ser	Ala	Phe	Leu	Thr	Val	Leu	Pro	Asp	Pro	Lys	Pro	Gln	Gly
			260					265					270		
Pro	Pro	Val	Ala	Ser	Ser	Ser	Ser	Ala	Thr	Ser	Leu	Pro	Trp	Pro	Val
		275					280					285			
Val	Ile	Gly	Ile	Pro	Ala	Gly	Ala	Val	Phe	Ile	Leu	Gly	Thr	Leu	Leu
	290					295					300				
Leu	Trp	Leu	Cys	Gln	Ala	Gln	Lys	Lys	Pro	Cys	Thr	Pro	Ala	Pro	Ala
305					310					315					320

Pro Pro Leu Pro Gly His Arg Pro Pro Gly Thr Ala Arg Asp Arg Ser
 325 330 335
 Gly Asp Lys Asp Leu Pro Ser Leu Ala Ala Leu Ser Ala Gly Pro Gly
 340 345 350
 Val Gly Leu Cys Glu Glu His Gly Ser Pro Ala Ala Pro Gln His Leu
 355 360 365
 Leu Gly Pro Gly Pro Val Ala Gly Pro Lys Leu Tyr Pro Lys Leu Tyr
 370 375 380
 Thr Asp Ile His Thr His Thr His Thr His Ser His Thr His Ser His
 385 390 395 400
 Val Glu Gly Lys Val His Gln His Ile His Tyr Gln Cys
 405 410

<210> 26
 <211> 876
 <212> DNA
 <213> Human

<400> 26
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 gcccggttgg gccgcactgt gcggctgcag tgcccagtgg agggggaccc gccgccgctg 180
 accatgtgga ccaaggatgg ccgcaccatc cacagcggct ggagccgctt ccgcgtgctg 240
 ccgcaggggc tgaagggtgaa gcaggtggag cgggaggatg ccggcgtgta cgtgtgcaag 300
 gccaccaacg gcttcggcag ccttagcgct aactacacc tcgtcgtgct ggatgacatt 360
 agcccaggga aggagagcct ggggcccgc acgtcctctg ggggtcaaga ggaccccgcc 420
 agccagcagt gggacccaaa accgcaaggg ccacctgtgg cctcctcgtc ctcggccact 480
 agcctgccgt ggcccggtgt catcggtatc ccagccggcg ctgtcttcat cctgggcacc 540
 ctgctcctgt ggctttgcca ggcccagaag aagccgtgca ccccgcgcc tgcccctccc 600
 ctgcttgggc accgcccgc ggggacggcc cgcgaccgca gcggagacaa ggaccttccc 660
 tcgttgcccg ccctcagcgc tggccctggt gtggggctgt gtgaggagca tgggtctccg 720
 gcagcccccc agcattact gggcccaggc ccagttgctg gccctaagtt gtacccccaa 780
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 ggcaagggtcc accagcacat ccactatcag tgctag 876

<210> 27
 <211> 291
 <212> PRT
 <213> Human

<400> 27
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 Gly Ala Phe Pro Pro Ala Ala Ala Ala Arg Gly Pro Pro Lys Met Ala
 20 25 30
 Asp Lys Val Val Pro Arg Gln Val Ala Arg Leu Gly Arg Thr Val Arg
 35 40 45
 Leu Gln Cys Pro Val Glu Gly Asp Pro Pro Pro Leu Thr Met Trp Thr
 50 55 60
 Lys Asp Gly Arg Thr Ile His Ser Gly Trp Ser Arg Phe Arg Val Leu
 65 70 75 80
 Pro Gln Gly Leu Lys Val Lys Gln Val Glu Arg Glu Asp Ala Gly Val
 85 90 95
 Tyr Val Cys Lys Ala Thr Asn Gly Phe Gly Ser Leu Ser Val Asn Tyr
 100 105 110
 Thr Leu Val Val Leu Asp Asp Ile Ser Pro Gly Lys Glu Ser Leu Gly
 115 120 125

Pro Asp Ser Ser Ser Gly Gly Gln Glu Asp Pro Ala Ser Gln Gln Trp
 130 135 140
 Asp Pro Lys Pro Gln Gly Pro Pro Val Ala Ser Ser Ser Ala Thr
 145 150 155 160
 Ser Leu Pro Trp Pro Val Val Ile Gly Ile Pro Ala Gly Ala Val Phe
 165 170 175
 Ile Leu Gly Thr Leu Leu Leu Trp Leu Cys Gln Ala Gln Lys Lys Pro
 180 185 190
 Cys Thr Pro Ala Pro Ala Pro Pro Leu Pro Gly His Arg Pro Pro Gly
 195 200 205
 Thr Ala Arg Asp Arg Ser Gly Asp Lys Asp Leu Pro Ser Leu Ala Ala
 210 215 220
 Leu Ser Ala Gly Pro Gly Val Gly Leu Cys Glu Glu His Gly Ser Pro
 225 230 235 240
 Ala Ala Pro Gln His Leu Leu Gly Pro Gly Pro Val Ala Gly Pro Lys
 245 250 255
 Leu Tyr Pro Lys Leu Tyr Thr Asp Ile His Thr His Thr His Thr His
 260 265 270
 Ser His Thr His Ser His Val Glu Gly Lys Val His Gln His Ile His
 275 280 285
 Tyr Gln Cys
 290

<210> 28
 <211> 1080
 <212> DNA
 <213> Human

<400> 28
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 gcccggttgg gccgcactgt gcggctgcag tgcccagtgg agggggaccc gccgccgctg 180
 accatgtgga ccaaggatgg ccgcaccatc cacagcggct ggagccgctt ccgcgtgctg 240
 ccgcagggggc tgaaggtgaa gcaggtggag cgggaggatg ccggcgtgta cgtgtgcaag 300
 gccaccaacg gcttcggcag ccttagcgtc aactacaccc tcgtcgtgct ggcacgaccg 360
 cgcttcacac agccctccaa gatgaggcgc cgggtgatcg cacggcccgt gggtagctcc 420
 gtgcggttca agtgcggtgg cagcggggcac cctcggcccg acatcacgtg gatgaaggac 480
 gaccaggcct tgacgcgccc agaggcgcgt gagcccagga agaagaagtg gacactgagc 540
 ctgaagaacc tgccggccgga ggacagcggc aaatacacct gccgcgtgtc gaaccgcgcg 600
 ggcgccatca acgccaccta caaggtggat gtgatccacc caaaaccgca agggccacct 660
 gtggcctcct cgtcctcggc cactagcctg ccgtggcccc tggtcatcgg catcccagcc 720
 ggcgctgtct tcatectggg caccctgctc ctgtggcttt gccaggccca gaagaagccg 780
 tgcacccccg cgctgcccc tcccctgcct gggcaccgcc cgccggggac ggcccgcgac 840
 cgcagcggag acaaggacct tccctcgttg gccgccctca gcgtggccc tggtgtgggg 900
 ctgtgtgagg agcatgggtc tccggcagcc ccccagcact tactggggcc aggcccagtt 960
 gctggcccta agttgtacct caaactctac acagacatcc acacacacac acacacacac 1020
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<210> 29
 <211> 359
 <212> PRT
 <213> Human

<400> 29
 Met Thr Pro Ser Pro Leu Leu Leu Leu Leu Leu Pro Pro Leu Leu Leu
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cgcggtggagt	acggcgccga	gggcccgcac	aactccacca	tcgatgtggg	cggccagaag	540
tttgtggtgc	tgcccacggg	tgacgtgtgg	tcgcgggccg	acggctccta	cctcaataag	600
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atcccagccg	gcgctgtctt	catcctgggc	accctgctcc	tgtggctttg	ccaggcccag	840
aagaagccgt	gcacccccgc	gcctgcccct	cccctgctct	ggcaccgccc	gccggggacg	900
gcccgcgacc	gcagcggaga	caaggacctt	ccctcgttgg	ccgccctcag	cgctggccct	960
ggtgtggggc	tgtgtgagga	gcatgggtct	ccggcagccc	cccagcactt	actggggcca	1020
ggcccagttg	ctggccctaa	gttgtacccc	aaactctaca	cagacatcca	cacacacaca	1080
cacacacact	ctcacacaca	ctcacacgtg	gagggcaagg	tccaccagca	catccactat	1140
cagtgtctag						1149

<210> 31
 <211> 382
 <212> PRT
 <213> Human

<400> 31

Met	Thr	Pro	Ser	Pro	Leu	Leu	Leu	Leu	Leu	Pro	Pro	Leu	Leu	Leu	
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			20					25					30		
Asp	Lys	Val	Val	Pro	Arg	Gln	Val	Ala	Arg	Leu	Gly	Arg	Thr	Val	Arg
		35					40					45			
Leu	Gln	Cys	Pro	Val	Glu	Gly	Asp	Pro	Pro	Pro	Leu	Thr	Met	Trp	Thr
		50				55					60				
Lys	Asp	Gly	Arg	Thr	Ile	His	Ser	Gly	Trp	Ser	Arg	Phe	Arg	Val	Leu
65					70				75					80	
Pro	Gln	Gly	Leu	Lys	Val	Lys	Gln	Val	Glu	Arg	Glu	Asp	Ala	Gly	Val
				85					90					95	
Tyr	Val	Cys	Lys	Ala	Thr	Asn	Gly	Phe	Gly	Ser	Leu	Ser	Val	Asn	Tyr
			100					105					110		
Thr	Leu	Val	Val	Leu	Glu	Arg	Thr	Arg	Ser	Lys	Pro	Val	Leu	Thr	Gly
		115					120					125			
Thr	His	Pro	Val	Asn	Thr	Thr	Val	Asp	Phe	Gly	Gly	Thr	Thr	Ser	Phe
					135						140				
Gln	Cys	Lys	Val	Arg	Ser	Asp	Val	Lys	Pro	Val	Ile	Gln	Trp	Leu	Lys
145				150					155					160	
Arg	Val	Glu	Tyr	Gly	Ala	Glu	Gly	Arg	His	Asn	Ser	Thr	Ile	Asp	Val
			165					170					175		
Gly	Gly	Gln	Lys	Phe	Val	Val	Leu	Pro	Thr	Gly	Asp	Val	Trp	Ser	Arg
			180					185				190			
Pro	Asp	Gly	Ser	Tyr	Leu	Asn	Lys	Leu	Leu	Ile	Thr	Arg	Ala	Arg	Gln
		195					200					205			
Asp	Asp	Ala	Gly	Met	Tyr	Ile	Cys	Leu	Gly	Ala	Asn	Thr	Met	Gly	Tyr
210				215							220				
Ser	Phe	Arg	Ser	Ala	Phe	Leu	Thr	Val	Leu	Pro	Asp	Pro	Lys	Pro	Gln
225				230						235				240	
Gly	Pro	Pro	Val	Ala	Ser	Ser	Ser	Ser	Ala	Thr	Ser	Leu	Pro	Trp	Pro
			245						250					255	
Val	Val	Ile	Gly	Ile	Pro	Ala	Gly	Ala	Val	Phe	Ile	Leu	Gly	Thr	Leu
			260					265				270			
Leu	Leu	Trp	Leu	Cys	Gln	Ala	Gln	Lys	Lys	Pro	Cys	Thr	Pro	Ala	Pro
		275					280					285			

Ala Pro Pro Leu Pro Gly His Arg Pro Pro Gly Thr Ala Arg Asp Arg
290 295 300
Ser Gly Asp Lys Asp Leu Pro Ser Leu Ala Ala Leu Ser Ala Gly Pro
305 310 315 320
Gly Val Gly Leu Cys Glu Glu His Gly Ser Pro Ala Ala Pro Gln His
325 330 335
Leu Leu Gly Pro Gly Pro Val Ala Gly Pro Lys Leu Tyr Pro Lys Leu
340 345 350
Tyr Thr Asp Ile His Thr His Thr His Thr His Ser His Thr His Ser
355 360 365
His Val Glu Gly Lys Val His Gln His Ile His Tyr Gln Cys
370 375 380

<210> 32
<211> 888
<212> DNA
<213> Human

<400> 32
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tcctctgggg gtcaagagga ccccgccagc cagcagtggg cacgaccgcg cttcacacag 180
ccctccaaga tgaggcgccg ggtgatcgca cggcccgtgg gtagctccgt gcggctcaag 240
tgcggtggcca gcgggcaccc tcggcccgcac atcacgtgga tgaaggacga ccaggccttg 300
acgcgccccag aggcgctga gccaggaag aagaagtgga cactgagcct gaagaacctg 360
cgcccgagg acagcggaac atacacctgc cgcgtgtcga accgcgcggg cgccatcaac 420
gccacctaca aggtggatgt gatccaccca aaaccgcaag ggccacctgt ggcctcctcg 480
tcctcgccca ctagcctgcc gtggcccgtg gtcacggca tcccagccgg cgtgtcttc 540
atcctgggca cctgtctcct gtggctttgc caggcccaga agaagccgtg ccccccgcg 600
cctgcccctc cctgacctg gcaccgccg cgggggacgg cccgcgaccg cagcggagac 660
aaggaccttc cctcgttggc cgccctcagc gctggccctg gtgtggggct gtgtgaggag 720
catgggtctc cggcagcccc ccagcactta ctgggcccag gccagttgc tggccctaag 780
ttgtacccca aactctacac agacatccac acacacacac acacacactc tcacacacac 840
tcacacgtgg agggcaaggt ccaccagcac atccactatc agtgctag 888

<210> 33
<211> 295
<212> PRT
<213> Human

<400> 33
Met Thr Pro Ser Pro Leu Leu Leu Leu Leu Leu Pro Pro Leu Leu Leu
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Gly Ala Phe Pro Pro Ala Ala Ala Ala Arg Asp Asp Ile Ser Pro Gly
20 25 30
Lys Glu Ser Leu Gly Pro Asp Ser Ser Ser Gly Gly Gln Glu Asp Pro
35 40 45
Ala Ser Gln Gln Trp Ala Arg Pro Arg Phe Thr Gln Pro Ser Lys Met
50 55 60
Arg Arg Arg Val Ile Ala Arg Pro Val Gly Ser Ser Val Arg Leu Lys
65 70 75 80
Cys Val Ala Ser Gly His Pro Arg Pro Asp Ile Thr Trp Met Lys Asp
85 90 95
Asp Gln Ala Leu Thr Arg Pro Glu Ala Glu Pro Arg Lys Lys Lys
100 105 110
Trp Thr Leu Ser Leu Lys Asn Leu Arg Pro Glu Asp Ser Gly Lys Tyr
115 120 125

Thr	Cys	Arg	Val	Ser	Asn	Arg	Ala	Gly	Ala	Ile	Asn	Ala	Thr	Tyr	Lys
130						135					140				
Val	Asp	Val	Ile	His	Pro	Lys	Pro	Gln	Gly	Pro	Pro	Val	Ala	Ser	Ser
145					150					155					160
Ser	Ser	Ala	Thr	Ser	Leu	Pro	Trp	Pro	Val	Val	Ile	Gly	Ile	Pro	Ala
				165					170					175	
Gly	Ala	Val	Phe	Ile	Leu	Gly	Thr	Leu	Leu	Leu	Trp	Leu	Cys	Gln	Ala
			180					185					190		
Gln	Lys	Lys	Pro	Cys	Thr	Pro	Ala	Pro	Ala	Pro	Pro	Leu	Pro	Gly	His
		195					200					205			
Arg	Pro	Pro	Gly	Thr	Ala	Arg	Asp	Arg	Ser	Gly	Asp	Lys	Asp	Leu	Pro
	210					215					220				
Ser	Leu	Ala	Ala	Leu	Ser	Ala	Gly	Pro	Gly	Val	Gly	Leu	Cys	Glu	Glu
225					230					235					240
His	Gly	Ser	Pro	Ala	Ala	Pro	Gln	His	Leu	Leu	Gly	Pro	Gly	Pro	Val
				245					250					255	
Ala	Gly	Pro	Lys	Leu	Tyr	Pro	Lys	Leu	Tyr	Thr	Asp	Ile	His	Thr	His
			260					265					270		
Thr	His	Thr	His	Ser	His	Thr	His	Ser	His	Val	Glu	Gly	Lys	Val	His
		275					280					285			
Gln	His	Ile	His	Tyr	Gln	Cys									
	290					295									

<210> 34

<211> 957

<212> DNA

<213> Human

<400> 34

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tcctctgggg	gtcaagagga	ccccgccagc	cagcagtggg	agcggacccg	ttccaagccc	180
gtgctcacag	gcacgcaccc	cgtgaacacg	acggtggact	tcggggggac	cacgtccttc	240
cagtgaagg	tgcgagcga	cgtgaagccg	gtgatccagt	ggctgaagcg	cgtggagtac	300
ggcgccgagg	gccgccacaa	ctccaccatc	gatgtgggcg	gccagaagtt	tgtggtgctg	360
cccacgggtg	acgtgtggtc	gcggcccagc	ggctcctacc	tcaataagct	gctcatcacc	420
cgtgcccgcg	aggacgatgc	gggcatgtac	atctgccttg	gcgccaacac	catgggtac	480
agcttcgcga	gcgccttctc	caccgtgctg	ccagacccaa	aaccgcaagg	gccacctgtg	540
gcctctcgt	cctcgggcac	tagcctgccc	tggcccgtgg	tcacggcat	cccagccggc	600
gctgtcttca	tcctgggcac	cctgctcctg	tggctttgcc	aggcccagaa	gaagccgtgc	660
accctccgcg	cctgcccctc	cctgcctggg	caccgcccgc	cggggacggc	ccgcgaccgc	720
agcggagaca	aggaccttcc	ctcggtggcc	gccctcagcg	ctggccctgg	tgtggggctg	780
tgtgaggagc	atgggtctcc	ggcagcccc	cagcacttac	tgggcccagg	cccagttgct	840
ggccctaagt	tgtaccccaa	actctacaca	gacatccaca	cacacacaca	cacacactct	900
cacacacact	cacacgtgga	gggcaaggtc	caccagcaca	tccactatca	gtgctag	957

<210> 35

<211> 318

<212> PRT

<213> Human

<400> 35

Met	Thr	Pro	Ser	Pro	Leu	Leu	Leu	Leu	Leu	Pro	Pro	Leu	Leu	Leu
1			5					10				15		
Gly	Ala	Phe	Pro	Pro	Ala	Ala	Ala	Ala	Arg	Asp	Asp	Ile	Ser	Pro
			20					25				30		
Lys	Glu	Ser	Leu	Gly	Pro	Asp	Ser	Ser	Ser	Gly	Gly	Gln	Glu	Asp
														Pro

ccgccgggga cggcccgcca ccgcagcgga gacaaggacc ttccctcggt ggccgccttc 960
 agcgctggcc ctggtgtggg gctgtgtgag gagcatgggt ctccggcagc cccccagcac 1020
 ttactgggga caggccagc tgctggccct aagttgtacc ccaaactcta cacagacatc 1080
 cacacacaca cacacacaca ctctcacaca cactcacacg tggagggcaa ggtccaccag 1140
 cacatccact atcagtgcta g 1161

<210> 37

<211> 386

<212> PRT

<213> Human

<400> 37

Met	Thr	Pro	Ser	Pro	Leu	Leu	Leu	Leu	Leu	Leu	Pro	Pro	Leu	Leu	Leu
1				5					10				15		
Gly	Ala	Phe	Pro	Pro	Ala	Ala	Ala	Ala	Arg	Ala	Arg	Pro	Arg	Phe	Thr
			20					25				30			
Gln	Pro	Ser	Lys	Met	Arg	Arg	Arg	Val	Ile	Ala	Arg	Pro	Val	Gly	Ser
		35					40					45			
Ser	Val	Arg	Leu	Lys	Cys	Val	Ala	Ser	Gly	His	Pro	Arg	Pro	Asp	Ile
	50					55					60				
Thr	Trp	Met	Lys	Asp	Asp	Gln	Ala	Leu	Thr	Arg	Pro	Glu	Ala	Ala	Glu
65				70						75					80
Pro	Arg	Lys	Lys	Lys	Trp	Thr	Leu	Ser	Leu	Lys	Asn	Leu	Arg	Pro	Glu
				85					90					95	
Asp	Ser	Gly	Lys	Tyr	Thr	Cys	Arg	Val	Ser	Asn	Arg	Ala	Gly	Ala	Ile
			100					105					110		
Asn	Ala	Thr	Tyr	Lys	Val	Asp	Val	Ile	Gln	Arg	Thr	Arg	Ser	Lys	Pro
		115					120					125			
Val	Leu	Thr	Gly	Thr	His	Pro	Val	Asn	Thr	Thr	Val	Asp	Phe	Gly	Gly
	130					135					140				
Thr	Thr	Ser	Phe	Gln	Cys	Lys	Val	Arg	Ser	Asp	Val	Lys	Pro	Val	Ile
145				150						155					160
Gln	Trp	Leu	Lys	Arg	Val	Glu	Tyr	Gly	Ala	Glu	Gly	Arg	His	Asn	Ser
			165					170						175	
Thr	Ile	Asp	Val	Gly	Gly	Gln	Lys	Phe	Val	Val	Leu	Pro	Thr	Gly	Asp
		180						185					190		
Val	Trp	Ser	Arg	Pro	Asp	Gly	Ser	Tyr	Leu	Asn	Lys	Leu	Leu	Ile	Thr
	195					200					205				
Arg	Ala	Arg	Gln	Asp	Asp	Ala	Gly	Met	Tyr	Ile	Cys	Leu	Gly	Ala	Asn
	210					215					220				
Thr	Met	Gly	Tyr	Ser	Phe	Arg	Ser	Ala	Phe	Leu	Thr	Val	Leu	Pro	Asp
225				230						235					240
Pro	Lys	Pro	Gln	Gly	Pro	Pro	Val	Ala	Ser	Ser	Ser	Ser	Ala	Thr	Ser
			245					250					255		
Leu	Pro	Trp	Pro	Val	Val	Ile	Gly	Ile	Pro	Ala	Gly	Ala	Val	Phe	Ile
		260					265						270		
Leu	Gly	Thr	Leu	Leu	Leu	Trp	Leu	Cys	Gln	Ala	Gln	Lys	Lys	Pro	Cys
	275					280						285			
Thr	Pro	Ala	Pro	Ala	Pro	Pro	Leu	Pro	Gly	His	Arg	Pro	Pro	Gly	Thr
	290					295					300				
Ala	Arg	Asp	Arg	Ser	Gly	Asp	Lys	Asp	Leu	Pro	Ser	Leu	Ala	Ala	Leu
305				310						315					320
Ser	Ala	Gly	Pro	Gly	Val	Gly	Leu	Cys	Glu	Glu	His	Gly	Ser	Pro	Ala
			325					330					335		
Ala	Pro	Gln	His	Leu	Leu	Gly	Pro	Gly	Pro	Val	Ala	Gly	Pro	Lys	Leu
		340					345					350			
Tyr	Pro	Lys	Leu	Tyr	Thr	Asp	Ile	His	Thr	His	Thr	His	Thr	His	Ser

Pro Ser Leu Ala Ala Leu Ser Ala Gly Pro Gly Val Gly Leu Cys Glu
195 200 205
Glu His Gly Ser Pro Ala Ala Pro Gln His Leu Leu Gly Pro Gly Pro
210 215 220
Val Ala Gly Pro Lys Leu Tyr Pro Lys Leu Tyr Thr Asp Ile His Thr
225 230 235 240
His Thr His Thr His Ser His Thr His Ser His Val Glu Gly Lys Val
245 250 255
His Gln His Ile His Tyr Gln Cys
260

<210> 40
<211> 603
<212> DNA
<213> Human

<400> 40
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tcctctgggg gtcaagagga ccccgccagc cagcagtggg acccaaaacc gcaagggcca 180
cctgtggcct cctcgtcctc ggccactagc ctgccgtggc ccgtgggtcat cggcatccca 240
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ccgtgcaccc ccgcgcctgc cctccccctg cctgggcacc gcccgccggg gacggcccgc 360
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gttgctggcc ctaagttgta ccccaaactc tacacagaca tccacacaca cacacacaca 540
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tag 603

<210> 41
<211> 200
<212> PRT
<213> Human

<400> 41
Met Thr Pro Ser Pro Leu Leu Leu Leu Leu Leu Pro Pro Leu Leu Leu
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20 25 30
Lys Glu Ser Leu Gly Pro Asp Ser Ser Ser Gly Gly Gln Glu Asp Pro
35 40 45
Ala Ser Gln Gln Trp Asp Pro Lys Pro Gln Gly Pro Pro Val Ala Ser
50 55 60
Ser Ser Ser Ala Thr Ser Leu Pro Trp Pro Val Val Ile Gly Ile Pro
65 70 75 80
Ala Gly Ala Val Phe Ile Leu Gly Thr Leu Leu Leu Trp Leu Cys Gln
85 90 95
Ala Gln Lys Lys Pro Cys Thr Pro Ala Pro Ala Pro Pro Leu Pro Gly
100 105 110
His Arg Pro Pro Gly Thr Ala Arg Asp Arg Ser Gly Asp Lys Asp Leu
115 120 125
Pro Ser Leu Ala Ala Leu Ser Ala Gly Pro Gly Val Gly Leu Cys Glu
130 135 140
Glu His Gly Ser Pro Ala Ala Pro Gln His Leu Leu Gly Pro Gly Pro
145 150 155 160
Val Ala Gly Pro Lys Leu Tyr Pro Lys Leu Tyr Thr Asp Ile His Thr
165 170 175

His Thr His Thr His Ser His Thr His Ser His Val Glu Gly Lys Val
180 185 190
His Gln His Ile His Tyr Gln Cys
195 200

<210> 42
<211> 807
<212> DNA
<213> Human

<400> 42
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gtgatcgcac ggcccgtggg tagctccgtg cggctcaagt gcgtggccag cgggcaccct 180
cggcccagaca tcacgtggat gaaggacgac caggccttga cgcgcccaga ggccgctgag 240
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tacacctgcc gcgtgtcgaa ccgcgcgggc gccatcaacg ccacctataa ggtggatgtg 360
atccacccaa aaccgcaagg gccacctgtg gcctcctcgt cctcggccac tagcctgccg 420
tggcccgtgg tcatcggcac cccagccggc gctgtcttca tcctgggcac cctgctcctg 480
tggcttttgc aggccagaa gaagccgtgc accccgcgc ctgcccctcc cctgcctggg 540
caccgcccgc cggggacggc ccgcgaccgc agcggagaca aggaccttcc ctcgttggcc 600
gccctcagcg ctggccctgg tgtggggctg tgtgaggagc atgggtctcc ggcagccccc 660
cagcacttac tgggcccagg cccagttgct ggccttaagt tgtaccccaa actctacaca 720
gacatccaca cacacacaca cacacactct cacacgtgga gggcaaggtc 780
caccagcaca tccactatca gtgctag 807

<210> 43
<211> 268
<212> PRT
<213> Human

<400> 43
Met Thr Pro Ser Pro Leu Leu Leu Leu Leu Leu Pro Pro Leu Leu Leu
1 5 10 15
Gly Ala Phe Pro Pro Ala Ala Ala Arg Ala Arg Pro Arg Phe Thr
20 25 30
Gln Pro Ser Lys Met Arg Arg Arg Val Ile Ala Arg Pro Val Gly Ser
35 40 45
Ser Val Arg Leu Lys Cys Val Ala Ser Gly His Pro Arg Pro Asp Ile
50 55 60
Thr Trp Met Lys Asp Asp Gln Ala Leu Thr Arg Pro Glu Ala Ala Glu
65 70 75 80
Pro Arg Lys Lys Lys Trp Thr Leu Ser Leu Lys Asn Leu Arg Pro Glu
85 90 95
Asp Ser Gly Lys Tyr Thr Cys Arg Val Ser Asn Arg Ala Gly Ala Ile
100 105 110
Asn Ala Thr Tyr Lys Val Asp Val Ile His Pro Lys Pro Gln Gly Pro
115 120 125
Pro Val Ala Ser Ser Ser Ser Ala Thr Ser Leu Pro Trp Pro Val Val
130 135 140
Ile Gly Ile Pro Ala Gly Ala Val Phe Ile Leu Gly Thr Leu Leu Leu
145 150 155 160
Trp Leu Cys Gln Ala Gln Lys Lys Pro Cys Thr Pro Ala Pro Ala Pro
165 170 175
Pro Leu Pro Gly His Arg Pro Pro Gly Thr Ala Arg Asp Arg Ser Gly
180 185 190

Asp Lys Asp Leu Pro Ser Leu Ala Ala Leu Ser Ala Gly Pro Gly Val
 195 200 205
 Gly Leu Cys Glu Glu His Gly Ser Pro Ala Ala Pro Gln His Leu Leu
 210 215 220
 Gly Pro Gly Pro Val Ala Gly Pro Lys Leu Tyr Pro Lys Leu Tyr Thr
 225 230 235 240
 Asp Ile His Thr His Thr His Thr His Ser His Thr His Ser His Val
 245 250 255
 Glu Gly Lys Val His Gln His Ile His Tyr Gln Cys
 260 265

<210> 44
 <211> 876
 <212> DNA
 <213> Human

<400> 44
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 ccggccgccg ccgcccagaga gcggaccctg tccaagcccc tgctcacagg cagcaccccc 120
 gtgaacacga cgggtggactt cgggggggacc acgtccttcc agtgcaaggt gcgcagcgac 180
 gtgaagccgg tgatccagtg gctgaagcgc gtggagtacg gcgccgaggg ccgccacaac 240
 tccaccatcg atgtgggcgg ccagaagttt gtggtgctgc ccacgggtga cgtgtggtcg 300
 cggcccagcg gctcctacct caataagctg ctcatcacc gtgcccgcca ggacgatgcg 360
 ggcattgata tctgccttgg cgccaacacc atgggctaca gcttccgcag cgccttcctc 420
 accgtgctgc cagaccctaa accgcaaggg ccacctgtgg cctcctcgtc ctcgggccact 480
 agcctgccgt ggcccgtggt catcggcctc ccagccggcg ctgtcttcat cctggggcacc 540
 ctgctcctgt ggctttgcca ggcccagaag aagccgtgca cccccgcgcc tgccccctccc 600
 ctgcttgggc accgcccgcc ggggacggcc cgcgaccgca gcggagacaa ggaccttccc 660
 tcgttggccg ccctcagcgc tggccctggt gtggggctgt gtgaggagca tgggtctccg 720
 gcagcccccc agcacttact gggcccaggc ccagttgctg gccctaagtt gtaccccaaa 780
 ctctacacag acatccacac acacacacac acacactctc acacacactc acacgtggag 840
 ggcaaggtcc accagcacat ccactatcag tgctag 876

<210> 45
 <211> 291
 <212> PRT

<213> Human

<400> 45
 Met Thr Pro Ser Pro Leu Leu Leu Leu Leu Leu Pro Pro Leu Leu Leu
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 Gly Ala Phe Pro Pro Ala Ala Ala Ala Arg Glu Arg Thr Arg Ser Lys
 20 25 30
 Pro Val Leu Thr Gly Thr His Pro Val Asn Thr Thr Val Asp Phe Gly
 35 40 45
 Gly Thr Thr Ser Phe Gln Cys Lys Val Arg Ser Asp Val Lys Pro Val
 50 55 60
 Ile Gln Trp Leu Lys Arg Val Glu Tyr Gly Ala Glu Gly Arg His Asn
 65 70 75 80
 Ser Thr Ile Asp Val Gly Gly Gln Lys Phe Val Val Leu Pro Thr Gly
 85 90 95
 Asp Val Trp Ser Arg Pro Asp Gly Ser Tyr Leu Asn Lys Leu Leu Ile
 100 105 110
 Thr Arg Ala Arg Gln Asp Asp Ala Gly Met Tyr Ile Cys Leu Gly Ala
 115 120 125
 Asn Thr Met Gly Tyr Ser Phe Arg Ser Ala Phe Leu Thr Val Leu Pro

130	135	140
Asp Pro Lys Pro Gln Gly	Pro Pro Val Ala Ser	Ser Ser Ser Ala Thr
145	150	155
Ser Leu Pro Trp	Pro Val Val Ile Gly Ile	Pro Ala Gly Ala Val Phe
165	170	175
Ile Leu Gly Thr	Leu Leu Leu Trp Leu Cys	Gln Ala Gln Lys Lys Pro
180	185	190
Cys Thr Pro Ala	Pro Ala Pro Pro Leu Pro	Gly His Arg Pro Pro Gly
195	200	205
Thr Ala Arg Asp	Arg Ser Gly Asp Lys Asp	Leu Pro Ser Leu Ala Ala
210	215	220
Leu Ser Ala Gly	Pro Gly Val Gly Leu Cys	Glu Glu His Gly Ser Pro
225	230	235
Ala Ala Pro Gln	His Leu Leu Gly Pro Gly	Pro Val Ala Gly Pro Lys
245	250	255
Leu Tyr Pro Lys	Leu Tyr Thr Asp Ile His	Thr His Thr His Thr His
260	265	270
Ser His Thr His	Ser His Val Glu Gly Lys	Val His Gln His Ile His
275	280	285
Tyr Gln Cys		
290		

<210> 46
 <211> 522
 <212> DNA
 <213> Human

<400> 46	
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ccggccgccg ccgcccagaga cccaaaaccg caagggccac ctgtggcctc ctcgtcctcg	120
gccactagcc tgccgtggcc cgtgggtcatc ggcatcccag ccggcgctgt cttcatcctg	180
ggcaccctgc tcctgtggct ttgccaggcc cagaagaagc cgtgcacccc cgcgcctgcc	240
cctcccctgc ctgggcaccg cccgccgggg acggcccgcg accgcagcgg agacaaggac	300
cttccctcgt tggccgccct cagcgtctggc cctgggtgtg ggctgtgtga ggagcatggg	360
tctccggcag cccccagca cttactgggc ccaggcccag ttgctggccc taagtgtac	420
cccaaactct acacagacat ccacacacac acacacacac actctcacac acactcacac	480
gtggagggca aggtccacca gcacatccac tatcagtgtc ag	522

<210> 47
 <211> 173
 <212> PRT
 <213> Human

<400> 47
Met Thr Pro Ser Pro Leu Leu Leu Leu Leu Leu Pro Pro Leu Leu Leu
1 5 10 15
Gly Ala Phe Pro Pro Ala Ala Ala Ala Arg Asp Pro Lys Pro Gln Gly
20 25 30
Pro Pro Val Ala Ser Ser Ser Ser Ala Thr Ser Leu Pro Trp Pro Val
35 40 45
Val Ile Gly Ile Pro Ala Gly Ala Val Phe Ile Leu Gly Thr Leu Leu
50 55 60
Leu Trp Leu Cys Gln Ala Gln Lys Lys Pro Cys Thr Pro Ala Pro Ala
65 70 75 80
Pro Pro Leu Pro Gly His Arg Pro Pro Gly Thr Ala Arg Asp Arg Ser
85 90 95
Gly Asp Lys Asp Leu Pro Ser Leu Ala Ala Leu Ser Ala Gly Pro Gly

		100						105						110						
Val	Gly	Leu	Cys	Glu	Glu	His	Gly	Ser	Pro	Ala	Ala	Pro	Gln	His	Leu					
		115						120					125							
Leu	Gly	Pro	Gly	Pro	Val	Ala	Gly	Pro	Lys	Leu	Tyr	Pro	Lys	Leu	Tyr					
		130					135						140							
Thr	Asp	Ile	His	Thr	His	Thr	His	Thr	His	Ser	His	Thr	His	Ser	His					
145					150					155					160					
Val	Glu	Gly	Lys	Val	His	Gln	His	Ile	His	Tyr	Gln	Cys								
			165					170												

<210> 48
 <211> 1072
 <212> DNA
 <213> Human

<400> 48

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ccggccgccg	ccgcccagag	ccccccaaag	atggcggaca	aggtggtccc	acggcaggtg	120
gcccggctgg	gccgcactgt	gcggctgcag	tgcccagtgg	agggggaccc	gccgccgctg	180
accatgtgga	ccaaggatgg	ccgcaccatc	cacagcggct	ggagccgctt	ccgcgtgctg	240
ccgcaggggc	tgaaggtgaa	gcaggtggag	cgggaggatg	ccggcgtgta	cgtgtgcaag	300
gccaccaacg	gcttcggcag	ccttagcgtc	aactacacc	tcgtcgtgct	ggatgacatt	360
agcccaggga	aggagagcct	ggggcccag	agctcctctg	ggggtcaaga	ggaccccgcc	420
agccagcagt	gggcacgacc	gcgcttcaca	cagccctcca	agatgaggcg	ccgggtgatc	480
gcacggcccc	tgggtagctc	cgtgcggctc	aagtgcgtgg	ccagcgggca	ccctcggccc	540
gacatcacgt	ggatgaagga	cgaccaggcc	ttgacgcgcc	cagaggccgc	tgagcccagg	600
aagaagaagt	ggacactgag	cctgaagaac	ctgcggcccg	aggacagcgg	caaatacacc	660
tgccgcgtgt	cgaaccgcgc	gggcgccatc	aacgccacct	acaaggtgga	tgtgatccag	720
cggaccgctt	ccaagcccgt	gctcacaggc	acgcaccccg	tgaacacgac	ggtggacttc	780
ggggggacca	cgctcttcca	gtgcaaggtg	cgcagcgacg	tgaagccggt	gatccagtgg	840
ctgaagcgcg	tggagtacgg	cgccgagggc	cgccacaact	ccaccatcga	tgtgggcggc	900
cagaagtttg	tgggtgctgc	cacgggtgac	gtgtggctgc	ggcccagcgg	ctcctacctc	960
aataagctgc	tcatcacccg	tgcccgccag	gacgatgcgg	gcatgtacat	ctgccttggc	1020
gccaacacca	tgggctacag	cttccgcagc	gccttctcct	ccgtgctgcc	ag	1072

<210> 49
 <211> 357
 <212> PRT
 <213> Human

<400> 49

Met	Thr	Pro	Ser	Pro	Leu	Leu	Leu	Leu	Leu	Pro	Pro	Leu	Leu	Leu	
1				5				10				15			
Gly	Ala	Phe	Pro	Pro	Ala	Ala	Ala	Ala	Arg	Gly	Pro	Pro	Lys	Met	Ala
			20					25				30			
Asp	Lys	Val	Val	Pro	Arg	Gln	Val	Ala	Arg	Leu	Gly	Arg	Thr	Val	Arg
		35					40					45			
Leu	Gln	Cys	Pro	Val	Glu	Gly	Asp	Pro	Pro	Pro	Leu	Thr	Met	Trp	Thr
		50				55					60				
Lys	Asp	Gly	Arg	Thr	Ile	His	Ser	Gly	Trp	Ser	Arg	Phe	Arg	Val	Leu
65					70				75					80	
Pro	Gln	Gly	Leu	Lys	Val	Lys	Gln	Val	Glu	Arg	Glu	Asp	Ala	Gly	Val
			85					90					95		
Tyr	Val	Cys	Lys	Ala	Thr	Asn	Gly	Phe	Gly	Ser	Leu	Ser	Val	Asn	Tyr
			100				105					110			
Thr	Leu	Val	Val	Leu	Asp	Asp	Ile	Ser	Pro	Gly	Lys	Glu	Ser	Leu	Gly
		115					120					125			

Pro	Asp	Ser	Ser	Ser	Gly	Gly	Gln	Glu	Asp	Pro	Ala	Ser	Gln	Gln	Trp
130						135					140				
Ala	Arg	Pro	Arg	Phe	Thr	Gln	Pro	Ser	Lys	Met	Arg	Arg	Arg	Val	Ile
145						150				155					160
Ala	Arg	Pro	Val	Gly	Ser	Ser	Val	Arg	Leu	Lys	Cys	Val	Ala	Ser	Gly
				165					170					175	
His	Pro	Arg	Pro	Asp	Ile	Thr	Trp	Met	Lys	Asp	Asp	Gln	Ala	Leu	Thr
			180					185					190		
Arg	Pro	Glu	Ala	Ala	Glu	Pro	Arg	Lys	Lys	Lys	Trp	Thr	Leu	Ser	Leu
		195					200					205			
Lys	Asn	Leu	Arg	Pro	Glu	Asp	Ser	Gly	Lys	Tyr	Thr	Cys	Arg	Val	Ser
	210					215					220				
Asn	Arg	Ala	Gly	Ala	Ile	Asn	Ala	Thr	Tyr	Lys	Val	Asp	Val	Ile	Gln
225					230					235					240
Arg	Thr	Arg	Ser	Lys	Pro	Val	Leu	Thr	Gly	Thr	His	Pro	Val	Asn	Thr
				245					250					255	
Thr	Val	Asp	Phe	Gly	Gly	Thr	Thr	Ser	Phe	Gln	Cys	Lys	Val	Arg	Ser
			260					265					270		
Asp	Val	Lys	Pro	Val	Ile	Gln	Trp	Leu	Lys	Arg	Val	Glu	Tyr	Gly	Ala
		275					280					285			
Glu	Gly	Arg	His	Asn	Ser	Thr	Ile	Asp	Val	Gly	Gly	Gln	Lys	Phe	Val
	290					295				300					
Val	Leu	Pro	Thr	Gly	Asp	Val	Trp	Ser	Arg	Pro	Asp	Gly	Ser	Tyr	Leu
305					310				315						320
Asn	Lys	Leu	Leu	Ile	Thr	Arg	Ala	Arg	Gln	Asp	Asp	Ala	Gly	Met	Tyr
				325					330					335	
Ile	Cys	Leu	Gly	Ala	Asn	Thr	Met	Gly	Tyr	Ser	Phe	Arg	Ser	Ala	Phe
			340					345					350		
Leu	Thr	Val	Leu	Pro											
			355												

<210> 50
 <211> 718
 <212> DNA
 <213> Human

<400> 50	
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cgggccgccg ccgcccaggg cccccaaag atggcggaca aggtgggtccc acggcagggtg	120
gccggctggg gccgcactgt gcggctgcag tgcccagtgagg ggggggaccc gccgccgctg	180
accatgtgga ccaaggatgg ccgcaccatc cacagcggct ggagccgctt ccgcgtgctg	240
ccgcagggggc tgaaggatgaa gcagggtggag cgggaggatg ccggcgtgta cgtgtgcaag	300
gccaccaacg gcttcggcag ccttagcgct aactacaccc tcgtcgtgct ggatgacatt	360
agcccagggg aggagagcct ggggcccagc agctcctctg ggggtcaaga ggaccccgcc	420
agccagcagt gggcacgacc gcgcttcaca cagccctcca agatgaggcg ccgggtgatc	480
gcacggcccc tgggtagctc cgtgctggct aagtgcgtgg ccagcgggca ccctcggccc	540
gacatcacgt ggatgaagga cgaccaggcc ttgacgcgcc cagaggccgc tgagcccagg	600
aagaagaagt ggacactgag cctgaagaac ctgctggccg aggacagcgg caaatacacc	660
tgccgcgtgt cgaaccgcgc gggcgccatc aacgccacct acaagggtgga tgtgatcc	718

<210> 51
 <211> 239
 <212> PRT
 <213> Human

<400> 51
 Met Thr Pro Ser Pro Leu Leu Leu Leu Leu Leu Pro Pro Leu Leu Leu

Met	Thr	Pro	Ser	Pro	Leu	Leu	Leu	Leu	Leu	Leu	Pro	Pro	Leu	Leu	Leu
1				5					10				15		
Gly	Ala	Phe	Pro	Pro	Ala	Ala	Ala	Ala	Arg	Gly	Pro	Pro	Lys	Met	Ala
			20					25					30		
Asp	Lys	Val	Val	Pro	Arg	Gln	Val	Ala	Arg	Leu	Gly	Arg	Thr	Val	Arg
		35					40					45			
Leu	Gln	Cys	Pro	Val	Glu	Gly	Asp	Pro	Pro	Pro	Leu	Thr	Met	Trp	Thr
	50					55					60				
Lys	Asp	Gly	Arg	Thr	Ile	His	Ser	Gly	Trp	Ser	Arg	Phe	Arg	Val	Leu
65					70				75					80	
Pro	Gln	Gly	Leu	Lys	Val	Lys	Gln	Val	Glu	Arg	Glu	Asp	Ala	Gly	Val
				85					90					95	
Tyr	Val	Cys	Lys	Ala	Thr	Asn	Gly	Phe	Gly	Ser	Leu	Ser	Val	Asn	Tyr
			100					105					110		
Thr	Leu	Val	Val	Leu	Asp	Asp	Ile	Ser	Pro	Gly	Lys	Glu	Ser	Leu	Gly
		115					120					125			
Pro	Asp	Ser	Ser	Ser	Gly	Gly	Gln	Glu	Asp	Pro	Ala	Ser	Gln	Gln	Trp
	130					135					140				
Glu	Arg	Thr	Arg	Ser	Lys	Pro	Val	Leu	Thr	Gly	Thr	His	Pro	Val	Asn
145					150					155				160	
Thr	Thr	Val	Asp	Phe	Gly	Gly	Thr	Thr	Ser	Phe	Gln	Cys	Lys	Val	Arg
			165						170					175	
Ser	Asp	Val	Lys	Pro	Val	Ile	Gln	Trp	Leu	Lys	Arg	Val	Glu	Tyr	Gly
			180					185					190		
Ala	Glu	Gly	Arg	His	Asn	Ser	Thr	Ile	Asp	Val	Gly	Gly	Gln	Lys	Phe
		195					200					205			
Val	Val	Leu	Pro	Thr	Gly	Asp	Val	Trp	Ser	Arg	Pro	Asp	Gly	Ser	Tyr
	210					215					220				
Leu	Asn	Lys	Leu	Leu	Ile	Thr	Arg	Ala	Arg	Gln	Asp	Asp	Ala	Gly	Met
225					230					235				240	
Tyr	Ile	Cys	Leu	Gly	Ala	Asn	Thr	Met	Gly	Tyr	Ser	Phe	Arg	Ser	Ala
			245						250					255	
Phe	Leu	Thr	Val	Leu	Pro										
			260												

<210> 54
 <211> 991
 <212> DNA
 <213> Human

<400> 54	
atgacgccga gccccctggt gctgctcctg ctgccgcgcg tgctgctggg ggccttccca	60
ccggccgccg ccgcccagg cccccaaag atggcggaca aggtgggtccc acggcagggtg	120
gcccggctgg gccgcaactg gcggctgcag tgcccagtgg agggggaccc gccgccgtg	180
accatgtgga ccaaggatgg ccgcaccatc cacagcggct ggagccgctt ccgcgtgctg	240
ccgcaggggc tgaaggatga gcagggtggag cgggaggatg ccggcgtgta cgtgtgcaag	300
gccaccaacg gcttcggcag ccttagcgct aactacaccc tcgtcgtgct ggcacgaccg	360
cgcttcacac agccctccaa gatgaggcgc cgggtgatcg cacggcccgt gggtagctcc	420
gtgcggctca agtgcgtagg cagcgggcac cctcggcccg acatcacgtg gatgaaggac	480
gaccaggcct tgacgcgccc agaggccgct gagcccagga agaagaagtg gacactgagc	540
ctgaagaacc tgccggccgga ggacagcggc aaatacacct gccgcgtgtc gaaccgcgcg	600
ggcgccatca acgccacct caaggtggat gtgatccagc ggaccggttc caagcccgtg	660
ctcacaggca cgcaccccgt gaacacgacg gtggacttcg gggggaccac gtccttccag	720
tgaaggatgc gcagcgacgt gaagccgggtg atccagtggc tgaagcgcgt ggagtacggc	780
gccgagggcc gccacaactc caccatcgat gtggggcgcc agaagtttgt ggtgctgcc	840
acgggtgacg tgtggtcgcg gcccgacggc tcctacctca ataagctgct catcaccgct	900
gcccgcacag acgatgcggg catgtacatc tgccttggcg ccaacacccat gggctacagc	960

ttccgcagcg ccttcctcac cgtgctgccca g

991

<210> 55
 <211> 330
 <212> PRT
 <213> Human

<400> 55
 Met Thr Pro Ser Pro Leu Leu Leu Leu Leu Leu Pro Pro Leu Leu Leu
 1 5 10 15
 Gly Ala Phe Pro Pro Ala Ala Ala Ala Arg Gly Pro Pro Lys Met Ala
 20 25 30
 Asp Lys Val Val Pro Arg Gln Val Ala Arg Leu Gly Arg Thr Val Arg
 35 40 45
 Leu Gln Cys Pro Val Glu Gly Asp Pro Pro Pro Leu Thr Met Trp Thr
 50 55 60
 Lys Asp Gly Arg Thr Ile His Ser Gly Trp Ser Arg Phe Arg Val Leu
 65 70 75 80
 Pro Gln Gly Leu Lys Val Lys Gln Val Glu Arg Glu Asp Ala Gly Val
 85 90 95
 Tyr Val Cys Lys Ala Thr Asn Gly Phe Gly Ser Leu Ser Val Asn Tyr
 100 105 110
 Thr Leu Val Val Leu Ala Arg Pro Arg Phe Thr Gln Pro Ser Lys Met
 115 120 125
 Arg Arg Arg Val Ile Ala Arg Pro Val Gly Ser Ser Val Arg Leu Lys
 130 135 140
 Cys Val Ala Ser Gly His Pro Arg Pro Asp Ile Thr Trp Met Lys Asp
 145 150 155 160
 Asp Gln Ala Leu Thr Arg Pro Glu Ala Ala Glu Pro Arg Lys Lys Lys
 165 170 175
 Trp Thr Leu Ser Leu Lys Asn Leu Arg Pro Glu Asp Ser Gly Lys Tyr
 180 185 190
 Thr Cys Arg Val Ser Asn Arg Ala Gly Ala Ile Asn Ala Thr Tyr Lys
 195 200 205
 Val Asp Val Ile Gln Arg Thr Arg Ser Lys Pro Val Leu Thr Gly Thr
 210 215 220
 His Pro Val Asn Thr Thr Val Asp Phe Gly Gly Thr Thr Ser Phe Gln
 225 230 235 240
 Cys Lys Val Arg Ser Asp Val Lys Pro Val Ile Gln Trp Leu Lys Arg
 245 250 255
 Val Glu Tyr Gly Ala Glu Gly Arg His Asn Ser Thr Ile Asp Val Gly
 260 265 270
 Gly Gln Lys Phe Val Val Leu Pro Thr Gly Asp Val Trp Ser Arg Pro
 275 280 285
 Asp Gly Ser Tyr Leu Asn Lys Leu Leu Ile Thr Arg Ala Arg Gln Asp
 290 295 300
 Asp Ala Gly Met Tyr Ile Cys Leu Gly Ala Asn Thr Met Gly Tyr Ser
 305 310 315 320
 Phe Arg Ser Ala Phe Leu Thr Val Leu Pro
 325 330

<210> 56
 <211> 799
 <212> DNA
 <213> Human

<400> 56

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tcctctgggg	gtcaagagga	ccccgccagc	cagcagtggg	cacgaccgcg	cttcacacag	180
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cggccggagg	acagcggcaa	atacacctgc	cgcgtgtcga	accgcgcggg	cgccatcaac	420
gccacctaca	aggtggatgt	gatccagcgg	acccgttcca	agcccgtgct	cacaggcacg	480
caccccgtag	acacgacggt	ggacttcggg	gggaccacgt	ccttccagt	caagggtgcgc	540
agcgacgtga	agccgggtgat	ccagtggctg	aagcgcgtgg	agtacggcgc	cgagggccgc	600
cacaactcca	ccatcgatgt	gggcggccag	aagtttgtgg	tgctgcccac	gggtgacgtg	660
tggtcgcggc	ccgacggctc	ctacctcaat	aagctgctca	tcacccgtgc	ccgccaggac	720
gatgcgggca	tgtacatctg	ccttggcgcc	aacaccatgg	gctacagctt	ccgcagcgcc	780
ttcctcaccg	tgctgccag					799

<210> 57

<211> 266

<212> PRT

<213> Human

<400> 57

Met	Thr	Pro	Ser	Pro	Leu	Leu	Leu	Leu	Leu	Pro	Pro	Leu	Leu	Leu
1				5				10				15		
Gly	Ala	Phe	Pro	Pro	Ala	Ala	Ala	Ala	Arg	Asp	Asp	Ile	Ser	Pro
			20					25				30		Gly
Lys	Glu	Ser	Leu	Gly	Pro	Asp	Ser	Ser	Ser	Gly	Gly	Gln	Glu	Asp
		35					40					45		Pro
Ala	Ser	Gln	Gln	Trp	Ala	Arg	Pro	Arg	Phe	Thr	Gln	Pro	Ser	Lys
	50					55					60			Met
Arg	Arg	Arg	Val	Ile	Ala	Arg	Pro	Val	Gly	Ser	Ser	Val	Arg	Leu
65					70				75					80
Cys	Val	Ala	Ser	Gly	His	Pro	Arg	Pro	Asp	Ile	Thr	Trp	Met	Lys
				85					90				95	Asp
Asp	Gln	Ala	Leu	Thr	Arg	Pro	Glu	Ala	Ala	Glu	Pro	Arg	Lys	Lys
		100						105					110	Lys
Trp	Thr	Leu	Ser	Leu	Lys	Asn	Leu	Arg	Pro	Glu	Asp	Ser	Gly	Lys
	115					120						125		Tyr
Thr	Cys	Arg	Val	Ser	Asn	Arg	Ala	Gly	Ala	Ile	Asn	Ala	Thr	Lys
	130				135						140			
Val	Asp	Val	Ile	Gln	Arg	Thr	Arg	Ser	Lys	Pro	Val	Leu	Thr	Gly
145				150					155					160
His	Pro	Val	Asn	Thr	Thr	Val	Asp	Phe	Gly	Gly	Thr	Thr	Ser	Phe
			165					170					175	Gln
Cys	Lys	Val	Arg	Ser	Asp	Val	Lys	Pro	Val	Ile	Gln	Trp	Leu	Lys
		180						185				190		Arg
Val	Glu	Tyr	Gly	Ala	Glu	Gly	Arg	His	Asn	Ser	Thr	Ile	Asp	Val
	195					200					205			Gly
Gly	Gln	Lys	Phe	Val	Val	Leu	Pro	Thr	Gly	Asp	Val	Trp	Ser	Arg
	210					215					220			Pro
Asp	Gly	Ser	Tyr	Leu	Asn	Lys	Leu	Leu	Ile	Thr	Arg	Ala	Arg	Gln
225				230					235					240
Asp	Ala	Gly	Met	Tyr	Ile	Cys	Leu	Gly	Ala	Asn	Thr	Met	Gly	Tyr
			245					250					255	Ser
Phe	Arg	Ser	Ala	Phe	Leu	Thr	Val	Leu	Pro					
		260						265						

<210> 58

<211> 433
 <212> DNA
 <213> Human

<400> 58
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 gcccggtgg gccgcactgt gcggctgcag tgcccagtg agggggaccc gccgccgctg 180
 accatgtgga ccaaggatgg ccgcaccatc cacagcggct ggagccgctt ccgcgtgctg 240
 ccgcaggggc tgaaggtgaa gcaggtggag cgggaggatg ccggcgtgta cgtgtgcaag 300
 gccaccaacg gcttcggcag ccttagcgtc aactacaccc tcgtcgtgct ggatgacatt 360
 agcccaggga aggagagcct ggggcccgcac agctcctctg ggggtcaaga ggacccccgc 420
 agccagcagt ggg 433

<210> 59
 <211> 144
 <212> PRT
 <213> Human

<400> 59
 Met Thr Pro Ser Pro Leu Leu Leu Leu Leu Leu Pro Pro Leu Leu Leu
 1 5 10 15
 Gly Ala Phe Pro Pro Ala Ala Ala Ala Arg Gly Pro Pro Lys Met Ala
 20 25 30
 Asp Lys Val Val Pro Arg Gln Val Ala Arg Leu Gly Arg Thr Val Arg
 35 40 45
 Leu Gln Cys Pro Val Glu Gly Asp Pro Pro Pro Leu Thr Met Trp Thr
 50 55 60
 Lys Asp Gly Arg Thr Ile His Ser Gly Trp Ser Arg Phe Arg Val Leu
 65 70 75 80
 Pro Gln Gly Leu Lys Val Lys Gln Val Glu Arg Glu Asp Ala Gly Val
 85 90 95
 Tyr Val Cys Lys Ala Thr Asn Gly Phe Gly Ser Leu Ser Val Asn Tyr
 100 105 110
 Thr Leu Val Val Leu Asp Asp Ile Ser Pro Gly Lys Glu Ser Leu Gly
 115 120 125
 Pro Asp Ser Ser Ser Gly Gly Gln Glu Asp Pro Ala Ser Gln Gln Trp
 130 135 140

<210> 60
 <211> 637
 <212> DNA
 <213> Human

<400> 60
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 ccggccgccg ccgcccagag ccccccaaag atggcggaca aggtgggtccc acggcaggtg 120
 gcccggtgg gccgcactgt gcggctgcag tgcccagtg agggggaccc gccgccgctg 180
 accatgtgga ccaaggatgg ccgcaccatc cacagcggct ggagccgctt ccgcgtgctg 240
 ccgcaggggc tgaaggtgaa gcaggtggag cgggaggatg ccggcgtgta cgtgtgcaag 300
 gccaccaacg gcttcggcag ccttagcgtc aactacaccc tcgtcgtgct ggcacgaccg 360
 cgcttcacac agccctccaa gatgagggcg cgggtgatcg cacggcccgt gggtagctcc 420
 gtgcggctca agtgcggtggc cagcgggcac cctcggccc agatcacgtg gatgaaggac 480
 gaccaggcct tgacgcgccc agaggccgct gagcccagga agaagaagtg gacactgagc 540
 ctgaagaacc tgccggccgga ggacagcggc aaatacacct gccgcgtgtc gaaccgcgcg 600
 ggcgccatca acgccaccta caaggtggat gtgatcc 637

<210> 61
 <211> 212
 <212> PRT
 <213> Human

<400> 61
 Met Thr Pro Ser Pro Leu Leu Leu Leu Leu Leu Pro Pro Leu Leu Leu
 1 5 10 15
 Gly Ala Phe Pro Pro Ala Ala Ala Ala Arg Gly Pro Pro Lys Met Ala
 20 25 30
 Asp Lys Val Val Pro Arg Gln Val Ala Arg Leu Gly Arg Thr Val Arg
 35 40 45
 Leu Gln Cys Pro Val Glu Gly Asp Pro Pro Pro Leu Thr Met Trp Thr
 50 55 60
 Lys Asp Gly Arg Thr Ile His Ser Gly Trp Ser Arg Phe Arg Val Leu
 65 70 75 80
 Pro Gln Gly Leu Lys Val Lys Gln Val Glu Arg Glu Asp Ala Gly Val
 85 90 95
 Tyr Val Cys Lys Ala Thr Asn Gly Phe Gly Ser Leu Ser Val Asn Tyr
 100 105 110
 Thr Leu Val Val Leu Ala Arg Pro Arg Phe Thr Gln Pro Ser Lys Met
 115 120 125
 Arg Arg Arg Val Ile Ala Arg Pro Val Gly Ser Ser Val Arg Leu Lys
 130 135 140
 Cys Val Ala Ser Gly His Pro Arg Pro Asp Ile Thr Trp Met Lys Asp
 145 150 155 160
 Asp Gln Ala Leu Thr Arg Pro Glu Ala Ala Glu Pro Arg Lys Lys Lys
 165 170 175
 Trp Thr Leu Ser Leu Lys Asn Leu Arg Pro Glu Asp Ser Gly Lys Tyr
 180 185 190
 Thr Cys Arg Val Ser Asn Arg Ala Gly Ala Ile Asn Ala Thr Tyr Lys
 195 200 205
 Val Asp Val Ile
 210

<210> 62
 <211> 706
 <212> DNA
 <213> Human

<400> 62
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 gcccggctgg gccgcactgt gcggctgcag tgcccagtgg agggggaccc gccgccgctg 180
 accatgtgga ccaaggatgg ccgcaccatc cacagcggct ggagccgctt ccgctgtgctg 240
 ccgcagggggc tgaaggtgaa gcaggtggag cgggaggatg ccggcgtgta cgtgtgcaag 300
 gccaccaacg gcttcggcag ccttagcgtc aactacaccc tcgtcgtgct ggagcggacc 360
 cggtccaagc ccgtgctcac aggcacgcac cccgtgaaca cgacgggtgga cttcggggggg 420
 accacgtcct tccagtcaa ggtgcgcagc gacgtgaagc cggatgatcca gtggctgaag 480
 cgcggtggagt acggcgccga gggccgccac aactccacca tcgatgtggg cggccagaag 540
 tttgtggtgc tgcccacggg tgacgtgtgg tcgcgggccc acggctccta cctcaataag 600
 ctgctcatca cccgtgcccg ccaggacgat gcgggcatgt acatctgcct tggcgccaac 660
 accatgggct acagcttccg cagcgccttc ctcaccgtgc tgccag 706

<210> 63
 <211> 235
 <212> PRT

<213> Human

<400> 63

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Met Thr Pro Ser Pro Leu Leu Leu Leu Leu Leu Pro Pro Leu Leu Leu
 1          5          10          15
Gly Ala Phe Pro Pro Ala Ala Ala Ala Arg Gly Pro Pro Lys Met Ala
 20          25          30
Asp Lys Val Val Pro Arg Gln Val Ala Arg Leu Gly Arg Thr Val Arg
 35          40          45
Leu Gln Cys Pro Val Glu Gly Asp Pro Pro Pro Leu Thr Met Trp Thr
 50          55          60
Lys Asp Gly Arg Thr Ile His Ser Gly Trp Ser Arg Phe Arg Val Leu
 65          70          75          80
Pro Gln Gly Leu Lys Val Lys Gln Val Glu Arg Glu Asp Ala Gly Val
 85          90          95
Tyr Val Cys Lys Ala Thr Asn Gly Phe Gly Ser Leu Ser Val Asn Tyr
 100         105         110
Thr Leu Val Val Leu Glu Arg Thr Arg Ser Lys Pro Val Leu Thr Gly
 115         120         125
Thr His Pro Val Asn Thr Thr Val Asp Phe Gly Gly Thr Thr Ser Phe
 130         135         140
Gln Cys Lys Val Arg Ser Asp Val Lys Pro Val Ile Gln Trp Leu Lys
 145         150         155         160
Arg Val Glu Tyr Gly Ala Glu Gly Arg His Asn Ser Thr Ile Asp Val
 165         170         175
Gly Gly Gln Lys Phe Val Val Leu Pro Thr Gly Asp Val Trp Ser Arg
 180         185         190
Pro Asp Gly Ser Tyr Leu Asn Lys Leu Leu Ile Thr Arg Ala Arg Gln
 195         200         205
Asp Asp Ala Gly Met Tyr Ile Cys Leu Gly Ala Asn Thr Met Gly Tyr
 210         215         220
Ser Phe Arg Ser Ala Phe Leu Thr Val Leu Pro
 225         230         235
```

<210> 64

<211> 445

<212> DNA

<213> Human

<400> 64

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tcctctgggg gtcaagagga ccccgccagc cagcagtggg caccgaccg cttcacacag    180
ccctccaaga tgaggcgccg ggtgatcgca cggcccgtgg gtagctccgt gcggtcaag    240
tgcgtggcca gcgggcaccc tcggcccgcac atcacgtgga tgaaggacga ccaggccttg    300
acgcgcccag aggccgctga gccaggaag aagaagtgga cactgagcct gaagaacctg    360
cggccggagg acagcggaac atacacctgc cgcgtgtcga accgcgcggg cgccatcaac    420
gccacctaca aggtggatgt gatcc                                445
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<210> 65

<211> 148

<212> PRT

<213> Human

<400> 65

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Met Thr Pro Ser Pro Leu Leu Leu Leu Leu Leu Pro Pro Leu Leu Leu
 1          5          10          15
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Gly Ala Phe Pro Pro Ala Ala Ala Ala Arg Asp Asp Ile Ser Pro Gly
 20 25 30
 Lys Glu Ser Leu Gly Pro Asp Ser Ser Ser Gly Gly Gln Glu Asp Pro
 35 40 45
 Ala Ser Gln Gln Trp Ala Arg Pro Arg Phe Thr Gln Pro Ser Lys Met
 50 55 60
 Arg Arg Arg Val Ile Ala Arg Pro Val Gly Ser Ser Val Arg Leu Lys
 65 70 75 80
 Cys Val Ala Ser Gly His Pro Arg Pro Asp Ile Thr Trp Met Lys Asp
 85 90 95
 Asp Gln Ala Leu Thr Arg Pro Glu Ala Ala Glu Pro Arg Lys Lys Lys
 100 105 110
 Trp Thr Leu Ser Leu Lys Asn Leu Arg Pro Glu Asp Ser Gly Lys Tyr
 115 120 125
 Thr Cys Arg Val Ser Asn Arg Ala Gly Ala Ile Asn Ala Thr Tyr Lys
 130 135 140
 Val Asp Val Ile
 145

<210> 66
 <211> 514
 <212> DNA
 <213> Human

<400> 66
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 ccggccgccg ccgcccagaga tgacattagc ccaggaagg agagcctggg gcccacagc 120
 tcctctgggg gtcaagagga ccccgccagc cagcagtggg agcggaccg ttccaagccc 180
 gtgctcacag gcacgcaccc cgtgaacacg acggtggact tcggggggac cacgtccttc 240
 cagtgaagg tgccgcagca cgtgaagccg gtgatccagt ggctgaagcg cgtggagtac 300
 ggccgcgagg gccgccacaa ctccaccatc gatgtggcg gccagaagt tgtggtgctg 360
 cccacgggtg acgtgtggtc gcggcccgac ggctcctacc tcaataagct gctcatcacc 420
 cgtgcccgcc aggacgatgc gggcatgtac atctgccttg gcgccaacac catgggctac 480
 agcttccgca ggccttccct caccgtgctg ccag 514

<210> 67
 <211> 171
 <212> PRT
 <213> Human

<400> 67
 Met Thr Pro Ser Pro Leu Leu Leu Leu Leu Leu Pro Pro Leu Leu Leu
 1 5 10 15
 Gly Ala Phe Pro Pro Ala Ala Ala Ala Arg Asp Asp Ile Ser Pro Gly
 20 25 30
 Lys Glu Ser Leu Gly Pro Asp Ser Ser Ser Gly Gly Gln Glu Asp Pro
 35 40 45
 Ala Ser Gln Gln Trp Glu Arg Thr Arg Ser Lys Pro Val Leu Thr Gly
 50 55 60
 Thr His Pro Val Asn Thr Thr Val Asp Phe Gly Gly Thr Thr Ser Phe
 65 70 75 80
 Gln Cys Lys Val Arg Ser Asp Val Lys Pro Val Ile Gln Trp Leu Lys
 85 90 95
 Arg Val Glu Tyr Gly Ala Glu Gly Arg His Asn Ser Thr Ile Asp Val
 100 105 110
 Gly Gly Gln Lys Phe Val Val Leu Pro Thr Gly Asp Val Trp Ser Arg
 115 120 125

Pro Asp Gly Ser Tyr Leu Asn Lys Leu Leu Ile Thr Arg Ala Arg Gln
 130 135 140
 Asp Asp Ala Gly Met Tyr Ile Cys Leu Gly Ala Asn Thr Met Gly Tyr
 145 150 155 160
 Ser Phe Arg Ser Ala Phe Leu Thr Val Leu Pro
 165 170

<210> 68
 <211> 718
 <212> DNA
 <213> Human

<400> 68
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 ccggccgccg ccgcccagac acgaccgcgc ttcacacagc cctccaagat gaggcgccgg 120
 gtgatcgcac ggcccgtggg tagctccgtg cggctcaagt gcgtggccag cgggcaccct 180
 cggcccagaca tcacgtggat gaaggacgac caggccttga cgcgcccaga ggccgctgag 240
 cccaggaaga agaagtggac actgagcctg aagaacctgc ggccggagga cagcggcaaa 300
 tacacctgcc gcgtgtcgaa ccgcgcgggc gccatcaacg ccacctacaa ggtggatgtg 360
 atccagcgga cccgttccaa gcccgctgctc acaggcacgc accccgtgaa cacgacggtg 420
 gacttcgggg ggaccacgtc cttccagtgc aaggtgcgca gcgacgtgaa gccggtgatc 480
 cagtggctga agcgcgtgga gtacggcgcc gagggccgcc acaactccac catcgatgtg 540
 ggccggccaga agtttgtggg gctgcccacg ggtgacgtgt ggtcgcggcc cgacggctcc 600
 tacctcaata agctgctcat caccctgcc cgccaggacg atgcgggcat gtacatctgc 660
 cttggcgcca acaccatggg ctacagcttc cgcagcgctt tcctcaccgt gctgccag 718

<210> 69
 <211> 239
 <212> PRT
 <213> Human

<400> 69
 Met Thr Pro Ser Pro Leu Leu Leu Leu Leu Leu Pro Pro Leu Leu Leu
 1 5 10 15
 Gly Ala Phe Pro Pro Ala Ala Ala Ala Arg Ala Arg Pro Arg Phe Thr
 20 25 30
 Gln Pro Ser Lys Met Arg Arg Arg Val Ile Ala Arg Pro Val Gly Ser
 35 40 45
 Ser Val Arg Leu Lys Cys Val Ala Ser Gly His Pro Arg Pro Asp Ile
 50 55 60
 Thr Trp Met Lys Asp Asp Gln Ala Leu Thr Arg Pro Glu Ala Ala Glu
 65 70 75 80
 Pro Arg Lys Lys Lys Trp Thr Leu Ser Leu Lys Asn Leu Arg Pro Glu
 85 90 95
 Asp Ser Gly Lys Tyr Thr Cys Arg Val Ser Asn Arg Ala Gly Ala Ile
 100 105 110
 Asn Ala Thr Tyr Lys Val Asp Val Ile Gln Arg Thr Arg Ser Lys Pro
 115 120 125
 Val Leu Thr Gly Thr His Pro Val Asn Thr Thr Val Asp Phe Gly Gly
 130 135 140
 Thr Thr Ser Phe Gln Cys Lys Val Arg Ser Asp Val Lys Pro Val Ile
 145 150 155 160
 Gln Trp Leu Lys Arg Val Glu Tyr Gly Ala Glu Gly Arg His Asn Ser
 165 170 175
 Thr Ile Asp Val Gly Gly Gln Lys Phe Val Val Leu Pro Thr Gly Asp
 180 185 190
 Val Trp Ser Arg Pro Asp Gly Ser Tyr Leu Asn Lys Leu Leu Ile Thr

	195					200						205							
Arg	Ala	Arg	Gln	Asp	Asp	Ala	Gly	Met	Tyr	Ile	Cys	Leu	Gly	Ala	Asn				
	210					215					220								
Thr	Met	Gly	Tyr	Ser	Phe	Arg	Ser	Ala	Phe	Leu	Thr	Val	Leu	Pro					
225					230					235									

<210> 70
 <211> 352
 <212> DNA
 <213> Human

<400> 70
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 gcccggtctg gccgcactgt gcggctgcag tgcccagtgg agggggaccc gccgccgctg 180
 accatgtgga ccaaggatgg ccgcaccatc cacagcggct ggagccgctt ccgcgtgctg 240
 ccgcaggggg tgaagggtgaa gcaggtggag cgggaggatg ccggcgtgta cgtgtgcaag 300
 gccaccaacg gcttcggcag ccttagcgtc aactacaccc tcgtcgtgct gg 352

<210> 71
 <211> 117
 <212> PRT
 <213> Human

<400> 71
 Met Thr Pro Ser Pro Leu Leu Leu Leu Leu Leu Pro Pro Leu Leu Leu
 1 5 10 15
 Gly Ala Phe Pro Pro Ala Ala Ala Ala Arg Gly Pro Pro Lys Met Ala
 20 25 30
 Asp Lys Val Val Pro Arg Gln Val Ala Arg Leu Gly Arg Thr Val Arg
 35 40 45
 Leu Gln Cys Pro Val Glu Gly Asp Pro Pro Pro Leu Thr Met Trp Thr
 50 55 60
 Lys Asp Gly Arg Thr Ile His Ser Gly Trp Ser Arg Phe Arg Val Leu
 65 70 75 80
 Pro Gln Gly Leu Lys Val Lys Gln Val Glu Arg Glu Asp Ala Gly Val
 85 90 95
 Tyr Val Cys Lys Ala Thr Asn Gly Phe Gly Ser Leu Ser Val Asn Tyr
 100 105 110
 Thr Leu Val Val Leu
 115

<210> 72
 <211> 160
 <212> DNA
 <213> Human

<400> 72
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 ccggccgccg ccgcccagag tgacattagc ccagggaagg agagcctggg gcccgacagc 120
 tcctctgggg gtcaagagga ccccgccagc cagcagtggg 160

<210> 73
 <211> 53
 <212> PRT
 <213> Human

<400> 73

Met Thr Pro Ser Pro Leu Leu Leu Leu Leu Leu Pro Pro Leu Leu Leu
1 5 10 15
Gly Ala Phe Pro Pro Ala Ala Ala Ala Arg Asp Asp Ile Ser Pro Gly
20 25 30
Lys Glu Ser Leu Gly Pro Asp Ser Ser Ser Gly Gly Gln Glu Asp Pro
35 40 45
Ala Ser Gln Gln Trp
50

<210> 74

<211> 364

<212> DNA

<213> Human

<400> 74

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ccggccgccg	ccgcccagagc	acgaccgcgc	ttcacacagc	cctccaagat	gaggcgccgg	120
gtgatcgcac	ggcccggtggg	tagctccgtg	cggctcaagt	gcgtggccag	cgggcaccct	180
cggcccagaca	tcacgtggat	gaaggacgac	caggccttga	cgcgcccaga	ggccgctgag	240
cccaggaaga	agaagtggac	actgagcctg	aagaacctgc	ggccggagga	cagcggcaaa	300
tacacctgcc	gcgtgtcgaa	ccgcgcgggc	gccatcaacg	ccacctacaa	ggtggatgtg	360
atcc						364

<210> 75

<211> 121

<212> PRT

<213> Human

<400> 75

Met Thr Pro Ser Pro Leu Leu Leu Leu Leu Leu Pro Pro Leu Leu Leu
1 5 10 15
Gly Ala Phe Pro Pro Ala Ala Ala Ala Arg Ala Arg Pro Arg Phe Thr
20 25 30
Gln Pro Ser Lys Met Arg Arg Arg Val Ile Ala Arg Pro Val Gly Ser
35 40 45
Ser Val Arg Leu Lys Cys Val Ala Ser Gly His Pro Arg Pro Asp Ile
50 55 60
Thr Trp Met Lys Asp Asp Gln Ala Leu Thr Arg Pro Glu Ala Ala Glu
65 70 75 80
Pro Arg Lys Lys Lys Trp Thr Leu Ser Leu Lys Asn Leu Arg Pro Glu
85 90 95
Asp Ser Gly Lys Tyr Thr Cys Arg Val Ser Asn Arg Ala Gly Ala Ile
100 105 110
Asn Ala Thr Tyr Lys Val Asp Val Ile
115 120

<210> 76

<211> 433

<212> DNA

<213> Human

<400> 76

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gtgaacacga	cggtggactt	cggggggacc	acgtccttcc	agtgaaggt	gcgcagcgac	180
gtgaagccgg	tgatccagtg	gctgaagcgc	gtggagtacg	gcgccgaggg	ccgccacaac	240

tccaccatcg atgtgggagg ccagaagttt gtggtgctgc ccacgggtga cgtgtgggtcg	300
cggcccgacg gctcctacct caataagctg ctcataccac gtgcccgcga ggacgatgcg	360
ggcatgtaca tctgccttgg cgccaacacc atgggctaca gcttccgcag cgccttcctc	420
accgtgctgc cag	433

<210> 77
 <211> 144
 <212> PRT
 <213> Human

<400> 77

Met	Thr	Pro	Ser	Pro	Leu	Leu	Leu	Leu	Leu	Leu	Pro	Pro	Leu	Leu	Leu
1				5					10				15		
Gly	Ala	Phe	Pro	Pro	Ala	Ala	Ala	Ala	Arg	Glu	Arg	Thr	Arg	Ser	Lys
			20					25					30		
Pro	Val	Leu	Thr	Gly	Thr	His	Pro	Val	Asn	Thr	Thr	Val	Asp	Phe	Gly
			35				40					45			
Gly	Thr	Thr	Ser	Phe	Gln	Cys	Lys	Val	Arg	Ser	Asp	Val	Lys	Pro	Val
	50					55					60				
Ile	Gln	Trp	Leu	Lys	Arg	Val	Glu	Tyr	Gly	Ala	Glu	Gly	Arg	His	Asn
65					70					75					80
Ser	Thr	Ile	Asp	Val	Gly	Gly	Gln	Lys	Phe	Val	Val	Leu	Pro	Thr	Gly
			85						90					95	
Asp	Val	Trp	Ser	Arg	Pro	Asp	Gly	Ser	Tyr	Leu	Asn	Lys	Leu	Leu	Ile
			100					105					110		
Thr	Arg	Ala	Arg	Gln	Asp	Asp	Ala	Gly	Met	Tyr	Ile	Cys	Leu	Gly	Ala
		115					120					125			
Asn	Thr	Met	Gly	Tyr	Ser	Phe	Arg	Ser	Ala	Phe	Leu	Thr	Val	Leu	Pro
	130					135					140				

<210> 78
 <211> 79
 <212> DNA
 <213> Human

<400> 78	
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ccggccgccg ccgcccag	79

<210> 79
 <211> 26
 <212> PRT
 <213> Human

<400> 79

Met	Thr	Pro	Ser	Pro	Leu	Leu	Leu	Leu	Leu	Pro	Pro	Leu	Leu	Leu
1				5					10				15	
Gly	Ala	Phe	Pro	Pro	Ala	Ala	Ala	Ala	Arg					
			20					25						

<210> 80
 <211> 1590
 <212> DNA
 <213> Mouse

<400> 80	
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cgactgtgc	ggctacagt	cccagtggag	ggggaccac	caccgttgac	catgtggacc	180
aaagatggcc	gcacaatcca	cagtggctgg	agccgcttcc	gtgtgctgcc	ccagggctctg	240
aaggtgaagg	aggtggaggc	cgaggatgcc	ggtgtttatg	tgtgcaaggc	caccaatggc	300
tttggcagcc	tcagcgtcaa	ctacactctc	atcatcatgg	atgatattag	tccaggggaag	360
gagagccctg	ggccaggtgg	ttcttcgggg	ggccaggagg	acccagccag	ccagcagtgg	420
gcacggcctc	gcttcacaca	gccctccaag	atgaggcgcc	gagtgattgc	acggcctgtg	480
ggtagctctg	tgcggtctaa	gtgtgtggcc	agtgggcacc	cacggccaga	catcatgtgg	540
atgaaggatg	accagacctt	gacgcattca	gaggctagt	aacacagaaa	gaagaagtgg	600
acactgagct	tgaagaacct	gaagcctgaa	gacagtggca	agtacacgtg	ccgtgtatct	660
aacaaggccg	gtgccatcaa	cgccacctac	aaagtggatg	taatccagcg	gactcgttcc	720
aagcctgtgc	tcacagggac	acaccctgtg	aacacaacgg	tggacttcgg	tgggacaacg	780
tccttccagt	gcaaggtgcg	cagtgcgtg	aagcctgtga	tccagtggct	gaagcgggtg	840
gagtacggct	ccgaggggacg	ccacaactcc	accattgatg	tgggtggcca	gaagtttgtg	900
gtgttgccca	cgggtgatgt	gtggtcacgg	cctgatggct	cctacctcaa	caagctgctc	960
atctctcggg	cccgccagga	tgatgctggc	atgtacatct	gcctaggtgc	aaataccatg	1020
ggctacagtt	tccgtagcgc	cttcctcact	gtattaccag	accccaaacc	tccagggcct	1080
cctatggctt	cttcacgtgc	atccacaagc	ctgccatggc	ctgtggtgat	cggcatccca	1140
gctggtgctg	tcttcacatc	aggcactgtg	ctgctctggc	tttgccagac	caagaagaag	1200
ccatgtgccc	cagcatctac	acttcctgtg	cctgggcata	gtccccagg	gacatcccg	1260
gaacgcagt	gtgacaagga	cctgcccctca	tgtgctgtgg	gcataatgtga	ggagcatgga	1320
tccgccatgg	ccccccagca	catcctggcc	tctggctcaa	ctgctggccc	caagctgtac	1380
cccaggtat	acacagatgt	gcacacacac	acacatacac	acacctgcac	tcacacgctc	1440
tcattgtggag	ggcaaggttc	atcaacacca	gcattgtccac	tatcagtgtc	aaatacagcg	1500
aatctccaag	cactgtgtcc	tgaggtaggc	atttgggggc	caaggcaaca	ggttgggaga	1560
attgagaaca	atggaggaag	agtatcttag				1590

<210> 81

<211> 529

<212> PRT

<213> Mouse

<400> 81

Met	Thr	Arg	Ser	Pro	Ala	Leu	Leu	Leu	Leu	Leu	Gly	Ala	Leu	Pro
1				5					10				15	
Ser	Ala	Glu	Ala	Arg	Gly	Pro	Pro	Arg	Met	Ala	Asp	Lys	Val	Val
		20					25					30		
Pro	Arg	Gln	Val	Ala	Arg	Leu	Gly	Arg	Thr	Val	Arg	Leu	Gln	Cys
		35					40					45		
Val	Glu	Gly	Asp	Pro	Pro	Pro	Leu	Thr	Met	Trp	Thr	Lys	Asp	Gly
		50				55					60			
Thr	Ile	His	Ser	Gly	Trp	Ser	Arg	Phe	Arg	Val	Leu	Pro	Gln	Gly
65					70				75					80
Lys	Val	Lys	Glu	Val	Glu	Ala	Glu	Asp	Ala	Gly	Val	Tyr	Val	Cys
				85					90					95
Ala	Thr	Asn	Gly	Phe	Gly	Ser	Leu	Ser	Val	Asn	Tyr	Thr	Leu	Ile
			100					105					110	
Met	Asp	Asp	Ile	Ser	Pro	Gly	Lys	Glu	Ser	Pro	Gly	Pro	Gly	Gly
		115					120					125		
Ser	Gly	Gly	Gln	Glu	Asp	Pro	Ala	Ser	Gln	Gln	Trp	Ala	Arg	Pro
		130				135					140			
Phe	Thr	Gln	Pro	Ser	Lys	Met	Arg	Arg	Arg	Val	Ile	Ala	Arg	Pro
145					150					155				160
Gly	Ser	Ser	Val	Arg	Leu	Lys	Cys	Val	Ala	Ser	Gly	His	Pro	Arg
				165				170					175	
Asp	Ile	Met	Trp	Met	Lys	Asp	Asp	Gln	Thr	Leu	Thr	His	Leu	Glu
				180				185					190	

Ser	Glu	His	Arg	Lys	Lys	Lys	Trp	Thr	Leu	Ser	Leu	Lys	Asn	Leu	Lys
		195					200					205			
Pro	Glu	Asp	Ser	Gly	Lys	Tyr	Thr	Cys	Arg	Val	Ser	Asn	Lys	Ala	Gly
	210					215					220				
Ala	Ile	Asn	Ala	Thr	Tyr	Lys	Val	Asp	Val	Ile	Gln	Arg	Thr	Arg	Ser
225					230					235					240
Lys	Pro	Val	Leu	Thr	Gly	Thr	His	Pro	Val	Asn	Thr	Thr	Val	Asp	Phe
				245					250					255	
Gly	Gly	Thr	Thr	Ser	Phe	Gln	Cys	Lys	Val	Arg	Ser	Asp	Val	Lys	Pro
			260					265					270		
Val	Ile	Gln	Trp	Leu	Lys	Arg	Val	Glu	Tyr	Gly	Ser	Glu	Gly	Arg	His
		275					280					285			
Asn	Ser	Thr	Ile	Asp	Val	Gly	Gly	Gln	Lys	Phe	Val	Val	Leu	Pro	Thr
	290					295					300				
Gly	Asp	Val	Trp	Ser	Arg	Pro	Asp	Gly	Ser	Tyr	Leu	Asn	Lys	Leu	Leu
305					310					315					320
Ile	Ser	Arg	Ala	Arg	Gln	Asp	Asp	Ala	Gly	Met	Tyr	Ile	Cys	Leu	Gly
			325					330						335	
Ala	Asn	Thr	Met	Gly	Tyr	Ser	Phe	Arg	Ser	Ala	Phe	Leu	Thr	Val	Leu
		340						345					350		
Pro	Asp	Pro	Lys	Pro	Pro	Gly	Pro	Met	Ala	Ser	Ser	Ser	Ser	Ser	Ser
	355						360					365			
Thr	Ser	Leu	Pro	Trp	Pro	Val	Val	Ile	Gly	Ile	Pro	Ala	Gly	Ala	Val
	370					375					380				
Phe	Ile	Leu	Gly	Thr	Val	Leu	Leu	Trp	Leu	Cys	Gln	Thr	Lys	Lys	Lys
385					390					395					400
Pro	Cys	Ala	Pro	Ala	Ser	Thr	Leu	Pro	Val	Pro	Gly	His	Arg	Pro	Pro
			405					410						415	
Gly	Thr	Ser	Arg	Glu	Arg	Ser	Gly	Asp	Lys	Asp	Leu	Pro	Ser	Leu	Ala
		420						425				430			
Val	Gly	Ile	Cys	Glu	Glu	His	Gly	Ser	Ala	Met	Ala	Pro	Gln	His	Ile
	435						440					445			
Leu	Ala	Ser	Gly	Ser	Thr	Ala	Gly	Pro	Lys	Leu	Tyr	Pro	Lys	Leu	Tyr
	450					455					460				
Thr	Asp	Val	His	Thr	His	Thr	His	Thr	His	Thr	Cys	Thr	His	Thr	Leu
465					470					475					480
Ser	Cys	Gly	Gly	Gln	Gly	Ser	Ser	Thr	Pro	Ala	Cys	Pro	Leu	Ser	Val
			485					490					495		
Leu	Asn	Thr	Ala	Asn	Leu	Gln	Ala	Leu	Cys	Pro	Glu	Val	Gly	Ile	Trp
		500						505				510			
Gly	Pro	Arg	Gln	Gln	Val	Gly	Arg	Ile	Glu	Asn	Asn	Gly	Gly	Arg	Val
	515						520					525			

Ser

<210> 82
 <211> 1236
 <212> DNA
 <213> Mouse

<400> 82																
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gcgcgaggac	ccccagaat	ggcagacaaa	gtggtccac	ggcaggtggc	ccgcctgggc											120
cgcactgtgc	ggctacagt	cccagtggag	ggggacccac	caccgttgac	catgtggacc											180
aaagatggcc	gcacaatcca	cagtggctgg	agccgcttcc	gtgtgctgcc	ccagggtctg											240
aaggtgaagg	aggtggaggc	cgaggatgcc	ggtgtttatg	tgtgcaaggc	caccaatggc											300
tttggcagcc	tcagcgtcaa	ctacactctc	atcatcatgg	atgatattag	tccaggggaag											360

gagagccctg	ggccagggtg	ttcttcgggg	ggccaggagg	acccagccag	ccagcagtgg	420
gcacggcctc	gcttcacaca	gccctccaag	atgaggcgcc	gagtgattgc	acggcctgtg	480
ggtagctctg	tgcggctcaa	gtgtgtggcc	agtgggcacc	cacggccaga	catcatgtgg	540
atgaaggatg	accagacctt	gacgcatcta	gaggctagt	aacacagaaa	gaagaagtgg	600
acactgagct	tgaagaacct	gaagcctgaa	gacagtggca	agtacacgtg	ccgtgtatct	660
aacaaggccg	gtgccatcaa	cgccacctac	aaagtggatg	taatccaccc	caaacctcca	720
gggcctccta	tggcttcttc	atcgatcatc	acaagcctgc	catggcctgt	ggtgatcggc	780
atcccagctg	gtgctgtctt	catcctaggc	actgtgctgc	tctggctttg	ccagaccaag	840
aagaagccat	gtgccccagc	atctacactt	cctgtgcctg	ggcatcgtcc	cccagggaca	900
ttccgagaac	gcagtgggtg	caaggacctg	ccctcattgg	ctgtgggcat	atgtgaggag	960
catggatccg	ccatggcccc	ccagcacatc	ctggcctctg	gctcaactgc	tggccccaag	1020
ctgtacccca	agctatacac	agatgtgcac	acacacacac	atacacacac	ctgcactcac	1080
acgctctcat	gtggagggca	aggttcatca	acaccagcat	gtccactatc	agtgctaaat	1140
acagcgaatc	tccaagcact	gtgtcctgag	gtaggcattt	gggggccaag	gcaacaggtt	1200
gggagaattg	agaacaatgg	aggaagagta	tcttag			1236

<210> 83
 <211> 411
 <212> PRT
 <213> Mouse

<400> 83

Met	Thr	Arg	Ser	Pro	Ala	Leu	Leu	Leu	Leu	Leu	Gly	Ala	Leu	Pro
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Ser	Ala	Glu	Ala	Ala	Arg	Gly	Pro	Pro	Arg	Met	Ala	Asp	Lys	Val
			20					25				30		
Pro	Arg	Gln	Val	Ala	Arg	Leu	Gly	Arg	Thr	Val	Arg	Leu	Gln	Cys
		35					40					45		
Val	Glu	Gly	Asp	Pro	Pro	Pro	Leu	Thr	Met	Trp	Thr	Lys	Asp	Gly
	50					55					60			
Thr	Ile	His	Ser	Gly	Trp	Ser	Arg	Phe	Arg	Val	Leu	Pro	Gln	Gly
65				70					75					80
Lys	Val	Lys	Glu	Val	Glu	Ala	Glu	Asp	Ala	Gly	Val	Tyr	Val	Cys
			85						90				95	
Ala	Thr	Asn	Gly	Phe	Gly	Ser	Leu	Ser	Val	Asn	Tyr	Thr	Leu	Ile
		100						105					110	
Met	Asp	Asp	Ile	Ser	Pro	Gly	Lys	Glu	Ser	Pro	Gly	Pro	Gly	Gly
	115						120					125		
Ser	Gly	Gly	Gln	Glu	Asp	Pro	Ala	Ser	Gln	Gln	Trp	Ala	Arg	Pro
	130					135					140			
Phe	Thr	Gln	Pro	Ser	Lys	Met	Arg	Arg	Arg	Val	Ile	Ala	Arg	Pro
145					150					155				160
Gly	Ser	Ser	Val	Arg	Leu	Lys	Cys	Val	Ala	Ser	Gly	His	Pro	Arg
			165						170				175	
Asp	Ile	Met	Trp	Met	Lys	Asp	Asp	Gln	Thr	Leu	Thr	His	Leu	Glu
	180							185				190		
Ser	Glu	His	Arg	Lys	Lys	Lys	Trp	Thr	Leu	Ser	Leu	Lys	Asn	Leu
	195						200					205		
Pro	Glu	Asp	Ser	Gly	Lys	Tyr	Thr	Cys	Arg	Val	Ser	Asn	Lys	Ala
	210					215						220		
Ala	Ile	Asn	Ala	Thr	Tyr	Lys	Val	Asp	Val	Ile	His	Pro	Lys	Pro
225					230					235				240
Gly	Pro	Pro	Met	Ala	Ser	Ser	Ser	Ser	Ser	Thr	Ser	Leu	Pro	Trp
			245						250				255	
Val	Val	Ile	Gly	Ile	Pro	Ala	Gly	Ala	Val	Phe	Ile	Leu	Gly	Thr
		260					265					270		
Leu	Leu	Trp	Leu	Cys	Gln	Thr	Lys	Lys	Lys	Pro	Cys	Ala	Pro	Ala

	275		280		285										
Thr	Leu	Pro	Val	Pro	Gly	His	Arg	Pro	Pro	Gly	Thr	Ser	Arg	Glu	Arg
	290					295					300				
Ser	Gly	Asp	Lys	Asp	Leu	Pro	Ser	Leu	Ala	Val	Gly	Ile	Cys	Glu	Glu
305					310					315					320
His	Gly	Ser	Ala	Met	Ala	Pro	Gln	His	Ile	Leu	Ala	Ser	Gly	Ser	Thr
				325					330					335	
Ala	Gly	Pro	Lys	Leu	Tyr	Pro	Lys	Leu	Tyr	Thr	Asp	Val	His	Thr	His
			340					345				350			
Thr	His	Thr	His	Thr	Cys	Thr	His	Thr	Leu	Ser	Cys	Gly	Gly	Gln	Gly
		355					360					365			
Ser	Ser	Thr	Pro	Ala	Cys	Pro	Leu	Ser	Val	Leu	Asn	Thr	Ala	Asn	Leu
	370					375					380				
Gln	Ala	Leu	Cys	Pro	Glu	Val	Gly	Ile	Trp	Gly	Pro	Arg	Gln	Gln	Val
385					390					395					400
Gly	Arg	Ile	Glu	Asn	Asn	Gly	Gly	Arg	Val	Ser					
				405				410							

<210> 84
 <211> 1305
 <212> DNA
 <213> Mouse

<400> 84

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gcgcgaggac	ccccagaat	ggcagacaaa	gtgggtccac	ggcagggtggc	ccgcctgggc	120
cgcactgtgc	ggctacagt	cccagtggag	ggggaccac	caccgttgac	catgtggacc	180
aaagatggcc	gcacaatcca	cagtggctgg	agccgcttc	gtgtgctgcc	ccagggtctg	240
aaggtgaagg	aggtggaggc	cgaggatgcc	ggtgtttatg	tgtgcaaggc	caccaatggc	300
tttggcagcc	tcagcgtcaa	ctacactctc	atcatcatgg	atgatattag	tccaggggaag	360
gagagccctg	ggccagggtg	ttcttcgggg	ggccaggagg	accagccag	ccagcagtgg	420
gagcggactc	gttccaagcc	tgtgctcaca	gggacacacc	ctgtgaacac	aacggtggac	480
ttcgggtggga	caacgtcctt	ccagtgcgaag	gtgcgcagtg	acgtgaagcc	tgtgatccag	540
tggctgaagc	gggtggagta	cggctccgag	ggacgccaca	actccaccat	tgatgtgggt	600
ggccagaagt	ttgtggtggt	gcccacgggt	gatgtgtggt	cacggcctga	tggctcctac	660
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aaacctccag	ggcctcctat	ggcttcttca	tcgtcatcca	caagcctgcc	atggcctgtg	840
gtgatcgga	tcccagctgg	tgtgtcttc	atcctaggca	ctgtgctgct	ctggctttgc	900
cagaccaaga	agaagccatg	tgccccagca	tctacacttc	ctgtgcctgg	gcatcgtccc	960
ccagggaacat	cccagagaacg	cagtgggtgac	aaggacctgc	cctcattggc	tgtgggcata	1020
tgtgaggagc	atggatccgc	catggccccc	cagcacatcc	tggcctctgg	ctcaactgct	1080
ggccccaagc	tgtaccccaa	gctatacaca	gatgtgcaca	cacacacaca	tacacacacc	1140
tgcactcaca	cgctctcatg	tggagggcaa	ggttcatcaa	caccagcatg	tccactatca	1200
gtgctaaata	cagcgaatct	ccaagcactg	tgtcctgagg	taggcatttg	ggggccaagg	1260
caacaggttg	ggagaattga	gaacaatgga	ggaagagtat	cttag		1305

<210> 85
 <211> 434
 <212> PRT
 <213> Mouse

<400> 85

Met	Thr	Arg	Ser	Pro	Ala	Leu	Leu	Leu	Leu	Leu	Gly	Ala	Leu	Pro	
1				5				10				15			
Ser	Ala	Glu	Ala	Ala	Arg	Gly	Pro	Pro	Arg	Met	Ala	Asp	Lys	Val	Val
			20				25					30			

Pro Arg Gln Val Ala Arg Leu Gly Arg Thr Val Arg Leu Gln Cys Pro
 35 40 45
 Val Glu Gly Asp Pro Pro Pro Leu Thr Met Trp Thr Lys Asp Gly Arg
 50 55 60
 Thr Ile His Ser Gly Trp Ser Arg Phe Arg Val Leu Pro Gln Gly Leu
 65 70 75 80
 Lys Val Lys Glu Val Glu Ala Glu Asp Ala Gly Val Tyr Val Cys Lys
 85 90 95
 Ala Thr Asn Gly Phe Gly Ser Leu Ser Val Asn Tyr Thr Leu Ile Ile
 100 105 110
 Met Asp Asp Ile Ser Pro Gly Lys Glu Ser Pro Gly Pro Gly Gly Ser
 115 120 125
 Ser Gly Gly Gln Glu Asp Pro Ala Ser Gln Gln Trp Glu Arg Thr Arg
 130 135 140
 Ser Lys Pro Val Leu Thr Gly Thr His Pro Val Asn Thr Thr Val Asp
 145 150 155 160
 Phe Gly Gly Thr Thr Ser Phe Gln Cys Lys Val Arg Ser Asp Val Lys
 165 170 175
 Pro Val Ile Gln Trp Leu Lys Arg Val Glu Tyr Gly Ser Glu Gly Arg
 180 185 190
 His Asn Ser Thr Ile Asp Val Gly Gly Gln Lys Phe Val Val Leu Pro
 195 200 205
 Thr Gly Asp Val Trp Ser Arg Pro Asp Gly Ser Tyr Leu Asn Lys Leu
 210 215 220
 Leu Ile Ser Arg Ala Arg Gln Asp Asp Ala Gly Met Tyr Ile Cys Leu
 225 230 235 240
 Gly Ala Asn Thr Met Gly Tyr Ser Phe Arg Ser Ala Phe Leu Thr Val
 245 250 255
 Leu Pro Asp Pro Lys Pro Pro Gly Pro Pro Met Ala Ser Ser Ser Ser
 260 265 270
 Ser Thr Ser Leu Pro Trp Pro Val Val Ile Gly Ile Pro Ala Gly Ala
 275 280 285
 Val Phe Ile Leu Gly Thr Val Leu Leu Trp Leu Cys Gln Thr Lys Lys
 290 295 300
 Lys Pro Cys Ala Pro Ala Ser Thr Leu Pro Val Pro Gly His Arg Pro
 305 310 315 320
 Pro Gly Thr Ser Arg Glu Arg Ser Gly Asp Lys Asp Leu Pro Ser Leu
 325 330 335
 Ala Val Gly Ile Cys Glu Glu His Gly Ser Ala Met Ala Pro Gln His
 340 345 350
 Ile Leu Ala Ser Gly Ser Thr Ala Gly Pro Lys Leu Tyr Pro Lys Leu
 355 360 365
 Tyr Thr Asp Val His Thr His Thr His Thr His Thr Cys Thr His Thr
 370 375 380
 Leu Ser Cys Gly Gly Gln Gly Ser Ser Thr Pro Ala Cys Pro Leu Ser
 385 390 395 400
 Val Leu Asn Thr Ala Asn Leu Gln Ala Leu Cys Pro Glu Val Gly Ile
 405 410 415
 Trp Gly Pro Arg Gln Gln Val Gly Arg Ile Glu Asn Asn Gly Gly Arg
 420 425 430
 Val Ser

<210> 86

<211> 1509

<212> DNA

<213> Mouse

<400> 86

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cgcactgtgc	ggctacagt	cccagtgag	ggggaccac	caccgttgac	catgtggacc	180
aaagatggcc	gcacaatcca	cagtggctgg	agccgcttcc	gtgtgctgcc	ccagggctcg	240
aaggtgaagg	aggtggaggc	cgaggatgcc	ggtgtttatg	tgtgcaaggc	caccaatggc	300
tttggcagcc	tcagcgtcaa	ctacactctc	atcatcatgg	cacggcctcg	cttcacacag	360
ccctccaaga	tgaggcgccg	agtgattgca	cggcctgtgg	gtagctctgt	gcggctcaag	420
tgtgtggcca	gtgggcaccc	acggccagac	atcatgtgga	tgaaggatga	ccagaccttg	480
acgcatctag	aggctagtga	acacagaaag	aagaagtgga	cactgagctt	gaagaacctg	540
aagcctgaag	acagtggcaa	gtacacgtgc	cgtgtatcta	acaaggccgg	tgccatcaac	600
gccacctaca	aagtggatgt	aatccagcgg	actcgttcca	agcctgtgct	cacagggaca	660
caccctgtga	acacaacggt	ggacttcggt	gggacaacgt	ccttccagtg	caaggtgcgc	720
agtgcagtga	agcctgtgat	ccagtggtcg	aagcgggtgg	agtacggctc	cgagggacgc	780
cacaactcca	ccattgatgt	gggtggccag	aagtttgtgg	tgttgcccac	gggtgatgtg	840
tggtcacggc	ctgatggctc	ctacctcaac	aagctgctca	tctctcgggc	ccgccaggat	900
gatgctggca	tgtacatctg	cctaggtgca	aataccatgg	gctacagttt	ccgtagcgcc	960
ttcctcactg	tattaccaga	ccccaaacct	ccagggcctc	ctatggcttc	ttcatcgtca	1020
tccacaagcc	tgccatggcc	tgtggtgatc	ggcatcccag	ctggtgctgt	cttcatecta	1080
ggcactgtgc	tgctctggct	ttgccagacc	aagaagaagc	catgtgcccc	agcatctaca	1140
cttcctgtgc	ctgggcatcg	tccccaggg	acatcccag	aacgcagtgg	tgacaaggac	1200
ctgcctcat	tggtgtggg	catatgtgag	gagcatggat	ccgccatggc	ccccagcac	1260
atcctggcct	ctggctcaac	tgctggcccc	aagctgtacc	ccaagctata	cacagatgtg	1320
cacacacaca	cacatacaca	cacctgcact	cacacgctct	catgtggagg	gcaaggttca	1380
tcaacaccag	catgtccact	atcagtgcta	aatacagcga	atctccaagc	actgtgtcct	1440
gaggtaggca	tttggggggc	aaggcaacag	gttgggagaa	ttgagaacaa	tggaggaaga	1500
gtatcttag						1509

<210> 87

<211> 502

<212> PRT

<213> Mouse

<400> 87

Met	Thr	Arg	Ser	Pro	Ala	Leu	Leu	Leu	Leu	Leu	Gly	Ala	Leu	Pro
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Ser	Ala	Glu	Ala	Arg	Gly	Pro	Pro	Arg	Met	Ala	Asp	Lys	Val	Val
			20				25				30			
Pro	Arg	Gln	Val	Ala	Arg	Leu	Gly	Arg	Thr	Val	Arg	Leu	Gln	Cys
		35					40				45			
Val	Glu	Gly	Asp	Pro	Pro	Pro	Leu	Thr	Met	Trp	Thr	Lys	Asp	Gly
	50					55					60			
Thr	Ile	His	Ser	Gly	Trp	Ser	Arg	Phe	Arg	Val	Leu	Pro	Gln	Gly
65					70				75					80
Lys	Val	Lys	Glu	Val	Glu	Ala	Glu	Asp	Ala	Gly	Val	Tyr	Val	Cys
			85					90					95	
Ala	Thr	Asn	Gly	Phe	Gly	Ser	Leu	Ser	Val	Asn	Tyr	Thr	Leu	Ile
		100					105					110		
Met	Ala	Arg	Pro	Arg	Phe	Thr	Gln	Pro	Ser	Lys	Met	Arg	Arg	Arg
	115						120				125			
Ile	Ala	Arg	Pro	Val	Gly	Ser	Ser	Val	Arg	Leu	Lys	Cys	Val	Ala
	130					135					140			
Gly	His	Pro	Arg	Pro	Asp	Ile	Met	Trp	Met	Lys	Asp	Asp	Gln	Thr
145					150					155				160
Thr	His	Leu	Glu	Ala	Ser	Glu	His	Arg	Lys	Lys	Lys	Trp	Thr	Leu

				165					170					175			
Leu	Lys	Asn	Leu	Lys	Pro	Glu	Asp	Ser	Gly	Lys	Tyr	Thr	Cys	Arg	Val		
			180					185					190				
Ser	Asn	Lys	Ala	Gly	Ala	Ile	Asn	Ala	Thr	Tyr	Lys	Val	Asp	Val	Ile		
		195					200					205					
Gln	Arg	Thr	Arg	Ser	Lys	Pro	Val	Leu	Thr	Gly	Thr	His	Pro	Val	Asn		
	210					215					220						
Thr	Thr	Val	Asp	Phe	Gly	Gly	Thr	Thr	Ser	Phe	Gln	Cys	Lys	Val	Arg		
225					230					235					240		
Ser	Asp	Val	Lys	Pro	Val	Ile	Gln	Trp	Leu	Lys	Arg	Val	Glu	Tyr	Gly		
			245					250					255				
Ser	Glu	Gly	Arg	His	Asn	Ser	Thr	Ile	Asp	Val	Gly	Gly	Gln	Lys	Phe		
	260						265					270					
Val	Val	Leu	Pro	Thr	Gly	Asp	Val	Trp	Ser	Arg	Pro	Asp	Gly	Ser	Tyr		
	275					280					285						
Leu	Asn	Lys	Leu	Leu	Ile	Ser	Arg	Ala	Arg	Gln	Asp	Asp	Ala	Gly	Met		
	290					295				300							
Tyr	Ile	Cys	Leu	Gly	Ala	Asn	Thr	Met	Gly	Tyr	Ser	Phe	Arg	Ser	Ala		
305				310					315					320			
Phe	Leu	Thr	Val	Leu	Pro	Asp	Pro	Lys	Pro	Pro	Gly	Pro	Pro	Met	Ala		
			325					330					335				
Ser	Ser	Ser	Ser	Ser	Thr	Ser	Leu	Pro	Trp	Pro	Val	Val	Ile	Gly	Ile		
			340				345					350					
Pro	Ala	Gly	Ala	Val	Phe	Ile	Leu	Gly	Thr	Val	Leu	Leu	Trp	Leu	Cys		
		355				360					365						
Gln	Thr	Lys	Lys	Lys	Pro	Cys	Ala	Pro	Ala	Ser	Thr	Leu	Pro	Val	Pro		
	370					375				380							
Gly	His	Arg	Pro	Pro	Gly	Thr	Ser	Arg	Glu	Arg	Ser	Gly	Asp	Lys	Asp		
385				390					395					400			
Leu	Pro	Ser	Leu	Ala	Val	Gly	Ile	Cys	Glu	Glu	His	Gly	Ser	Ala	Met		
			405					410					415				
Ala	Pro	Gln	His	Ile	Leu	Ala	Ser	Gly	Ser	Thr	Ala	Gly	Pro	Lys	Leu		
		420					425					430					
Tyr	Pro	Lys	Leu	Tyr	Thr	Asp	Val	His	Thr	His	Thr	His	Thr	His	Thr		
	435					440					445						
Cys	Thr	His	Thr	Leu	Ser	Cys	Gly	Gly	Gln	Gly	Ser	Ser	Thr	Pro	Ala		
	450					455				460							
Cys	Pro	Leu	Ser	Val	Leu	Asn	Thr	Ala	Asn	Leu	Gln	Ala	Leu	Cys	Pro		
465					470				475					480			
Glu	Val	Gly	Ile	Trp	Gly	Pro	Arg	Gln	Gln	Val	Gly	Arg	Ile	Glu	Asn		
			485					490					495				
Asn	Gly	Gly	Arg	Val	Ser												
			500														

<210> 88
 <211> 1317
 <212> DNA
 <213> Mouse

<400> 88																	
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gcgcgagatg	atattagtcc	agggaaggag	agccctgggc	caggtgggtc	ttcggggggc											120	
caggaggacc	cagccagcca	gcagtgggca	cggcctcgct	tcacacagcc	ctccaagatg											180	
aggcgccgag	tgattgcacg	gcctgtgggt	agctctgtgc	ggctcaagtg	tgtggccagt											240	
gggcacccac	ggccagacat	catgtggatg	aaggatgacc	agaccttgac	gcattctagag											300	
gctagtgaac	acagaaagaa	gaagtggaca	ctgagcttga	agaacctgaa	gcctgaagac											360	
agtggaagt	acacgtgccg	tgtatctaac	aaggccggtg	ccatcaacgc	cacctacaaa											420	

gtggatgtaa	tccagcggac	tcgttccaag	cctgtgctca	cagggacaca	ccctgtgaac	480
acaacggtgg	acttcggtgg	gacaacgtcc	ttccagtgc	aggtgcgcag	tgacgtgaag	540
cctgtgatcc	agtggctgaa	gcgggtggag	tacggctccg	agggacgcca	caactccacc	600
attgatgtgg	gtggccagaa	gtttgtggtg	ttgcccacgg	gtgatgtgtg	gtcacggcct	660
gatggctcct	acctcaacaa	gctgctcatc	tctcgggccc	gccaggatga	tgctggcatg	720
tacatctgcc	taggtgcaaa	taccatgggc	tacagtttcc	gtagcgcctt	cctcactgta	780
ttaccagacc	ccaaacctcc	agggcctcct	atggcttctt	catcgtcatc	cacaagcctg	840
ccatggcctg	tggtgatcgg	catcccagct	ggtgctgtct	tcatcctagg	cactgtgctg	900
ctctggcttt	gccagaccaa	gaagaagcca	tgtgccccag	catctacact	tcctgtgcct	960
gggcatcgct	ccccagggac	atccccgagaa	cgcagtgggtg	acaaggacct	gccctcattg	1020
gctgtgggca	tatgtgagga	gcatggatcc	gccatggccc	cccagcacat	cctggcctct	1080
ggctcaactg	ctggcccca	gctgtacccc	aagctataca	cagatgtgca	cacacacaca	1140
catacacaca	cctgcactca	cacgctctca	tgtggagggc	aaggttcatc	aacaccagca	1200
tgtccactat	cagtgtctaaa	tacagcgaat	ctccaagcac	tgtgtcctga	ggtaggcatt	1260
tgggggccaa	ggcaacaggt	tgggagaatt	gagaacaatg	gaggaagagt	atcttag	1317

<210> 89

<211> 438

<212> PRT

<213> Mouse

<400> 89

Met	Thr	Arg	Ser	Pro	Ala	Leu	Leu	Leu	Leu	Leu	Gly	Ala	Leu	Pro
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Ser	Ala	Glu	Ala	Ala	Arg	Asp	Asp	Ile	Ser	Pro	Gly	Lys	Glu	Ser
			20					25					30	Pro
Gly	Pro	Gly	Gly	Ser	Ser	Gly	Gly	Gln	Glu	Asp	Pro	Ala	Ser	Gln
		35					40					45		Gln
Trp	Ala	Arg	Pro	Arg	Phe	Thr	Gln	Pro	Ser	Lys	Met	Arg	Arg	Val
	50					55					60			
Ile	Ala	Arg	Pro	Val	Gly	Ser	Ser	Val	Arg	Leu	Lys	Cys	Val	Ala
65					70					75				80
Gly	His	Pro	Arg	Pro	Asp	Ile	Met	Trp	Met	Lys	Asp	Asp	Gln	Thr
				85					90				95	Leu
Thr	His	Leu	Glu	Ala	Ser	Glu	His	Arg	Lys	Lys	Lys	Trp	Thr	Leu
		100						105					110	Ser
Leu	Lys	Asn	Leu	Lys	Pro	Glu	Asp	Ser	Gly	Lys	Tyr	Thr	Cys	Arg
	115						120					125		Val
Ser	Asn	Lys	Ala	Gly	Ala	Ile	Asn	Ala	Thr	Tyr	Lys	Val	Asp	Val
	130					135					140			Ile
Gln	Arg	Thr	Arg	Ser	Lys	Pro	Val	Leu	Thr	Gly	Thr	His	Pro	Val
145					150					155				160
Thr	Thr	Val	Asp	Phe	Gly	Gly	Thr	Thr	Ser	Phe	Gln	Cys	Lys	Val
			165						170					175
Ser	Asp	Val	Lys	Pro	Val	Ile	Gln	Trp	Leu	Lys	Arg	Val	Glu	Tyr
		180						185				190		Gly
Ser	Glu	Gly	Arg	His	Asn	Ser	Thr	Ile	Asp	Val	Gly	Gly	Gln	Lys
	195						200				205			Phe
Val	Val	Leu	Pro	Thr	Gly	Asp	Val	Trp	Ser	Arg	Pro	Asp	Gly	Ser
	210					215					220			Tyr
Leu	Asn	Lys	Leu	Leu	Ile	Ser	Arg	Ala	Arg	Gln	Asp	Asp	Ala	Gly
225					230					235				240
Tyr	Ile	Cys	Leu	Gly	Ala	Asn	Thr	Met	Gly	Tyr	Ser	Phe	Arg	Ser
			245						250					255
Phe	Leu	Thr	Val	Leu	Pro	Asp	Pro	Lys	Pro	Pro	Gly	Pro	Pro	Met
			260					265					270	Ala
Ser	Ser	Ser	Ser	Ser	Thr	Ser	Leu	Pro	Trp	Pro	Val	Val	Ile	Gly

275	280	285
Pro Ala Gly Ala Val Phe Ile Leu Gly Thr Val Leu Leu Trp Leu Cys		
290	295	300
Gln Thr Lys Lys Lys Pro Cys Ala Pro Ala Ser Thr Leu Pro Val Pro		
305	310	315
Gly His Arg Pro Pro Gly Thr Ser Arg Glu Arg Ser Gly Asp Lys Asp		
	325	330
Leu Pro Ser Leu Ala Val Gly Ile Cys Glu Glu His Gly Ser Ala Met		
	340	345
Ala Pro Gln His Ile Leu Ala Ser Gly Ser Thr Ala Gly Pro Lys Leu		
	355	360
Tyr Pro Lys Leu Tyr Thr Asp Val His Thr His Thr His Thr His Thr		
	370	375
Cys Thr His Thr Leu Ser Cys Gly Gly Gln Gly Ser Ser Thr Pro Ala		
385	390	395
Cys Pro Leu Ser Val Leu Asn Thr Ala Asn Leu Gln Ala Leu Cys Pro		
	405	410
Glu Val Gly Ile Trp Gly Pro Arg Gln Gln Val Gly Arg Ile Glu Asn		
	420	425
Asn Gly Gly Arg Val Ser		430
435		

<210> 90

<211> 951

<212> DNA

<213> Mouse

<400> 90

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gcgcgaggac	cccccaagaat	ggcagacaaa	gtggtcccac	ggcaggtggc	ccgcctgggc	120
cgcactgtgc	ggctacagtg	cccagtggag	ggggaccac	caccgttgac	catgtggacc	180
aaagatggcc	gcacaatcca	cagtggctgg	agccgcttcc	gtgtgctgcc	ccagggctctg	240
aaggtgaagg	aggtggaggc	cgaggatgcc	ggtgtttatg	tgtgcaaggc	caccaatggc	300
tttggcagcc	tcagcgtcaa	ctacactctc	atcatcatgg	atgatattag	tccaggggaag	360
gagagccctg	ggccagggtg	ttcttcgggg	ggccaggagg	acccagccag	ccagcagtgg	420
gaccccaaac	ctccagggcc	tcctatggct	tcttcacgt	catccacaag	cctgccatgg	480
cctgtggtga	tcggcatccc	agctggtgct	gtcttcaccc	taggcactgt	gctgctctgg	540
ctttgccaga	ccaagaagaa	gccatgtgcc	cagacatcta	cacttcctgt	gcctgggcat	600
cgtccccgag	ggacatcccc	agaacgcagt	ggtgacaagg	acctgccctc	attggctgtg	660
ggcatatgtg	aggagcatgg	atccgccatg	gccccccagc	acatcctggc	ctctggctca	720
actgctggcc	ccaagctgta	ccccaaagcta	tacacagatg	tgcacacaca	cacacataca	780
cacacctgca	ctcacacgct	ctcatgtgga	gggcaagggt	catcaacacc	agcatgtcca	840
ctatcagtgc	taaatacagc	gaatctccaa	gcactgtgtc	ctgaggtagg	catttggggg	900
ccaaggcaac	aggttggggag	aattgagaac	aatggaggaa	gagtatctta	g	951

<210> 91

<211> 316

<212> PRT

<213> Mouse

<400> 91

Met Thr Arg Ser Pro Ala Leu Leu Leu Leu Leu Gly Ala Leu Pro	
1	5
Ser Ala Glu Ala Arg Gly Pro Pro Arg Met Ala Asp Lys Val Val	
	20
Pro Arg Gln Val Ala Arg Leu Gly Arg Thr Val Arg Leu Gln Cys Pro	
	25
	30

35	40	45
Val Glu Gly Asp Pro Pro Pro	Leu Thr Met Trp Thr	Lys Asp Gly Arg
50	55	60
Thr Ile His Ser Gly Trp Ser	Arg Phe Arg Val	Leu Pro Gln Gly Leu
65	70	75
Lys Val Lys Glu Val Glu Ala	Glu Asp Ala Gly	Val Tyr Val Cys Lys
85	90	95
Ala Thr Asn Gly Phe Gly Ser	Leu Ser Val Asn Tyr	Thr Leu Ile Ile
100	105	110
Met Asp Asp Ile Ser Pro Gly	Lys Glu Ser Pro Gly	Pro Gly Gly Ser
115	120	125
Ser Gly Gly Gln Glu Asp Pro	Ala Ser Gln Gln Trp	Asp Pro Lys Pro
130	135	140
Pro Gly Pro Pro Met Ala Ser	Ser Ser Ser Ser	Thr Ser Leu Pro Trp
145	150	155
Pro Val Val Ile Gly Ile Pro	Ala Gly Ala Val	Phe Ile Leu Gly Thr
165	170	175
Val Leu Leu Trp Leu Cys Gln	Thr Lys Lys Lys	Pro Cys Ala Pro Ala
180	185	190
Ser Thr Leu Pro Val Pro Gly	His Arg Pro Pro	Gly Thr Ser Arg Glu
195	200	205
Arg Ser Gly Asp Lys Asp Leu	Pro Ser Leu Ala	Val Gly Ile Cys Glu
210	215	220
Glu His Gly Ser Ala Met Ala	Pro Gln His Ile	Leu Ala Ser Gly Ser
225	230	235
Thr Ala Gly Pro Lys Leu Tyr	Pro Lys Leu Tyr	Thr Asp Val His Thr
245	250	255
His Thr His Thr His Thr Cys	Thr His Thr Leu	Ser Cys Gly Gly Gln
260	265	270
Gly Ser Ser Thr Pro Ala Cys	Pro Leu Ser Val	Leu Asn Thr Ala Asn
275	280	285
Leu Gln Ala Leu Cys Pro Glu	Val Gly Ile Trp	Gly Pro Arg Gln Gln
290	295	300
Val Gly Arg Ile Glu Asn Asn	Gly Gly Arg Val	Ser
305	310	315

<210> 92

<211> 1155

<212> DNA

<213> Mouse

<400> 92

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gcgcgaggac	ccccagaat	ggcagacaaa	gtgggtcccac	ggcaggtggc	ccgcctgggc	120
cgactgtgc	ggctacagt	cccagtggag	ggggaccac	caccgttgac	catgtggacc	180
aaagatggcc	gcacaatcca	cagtggctgg	agccgcttc	gtgtgctgcc	ccagggtctg	240
aaggtgaagg	aggtggaggc	cgaggatgcc	ggtgtttatg	tgtgcaaggc	caccaatggc	300
tttggcagcc	tcagcgtcaa	ctacactctc	atcatcatgg	cacggcctcg	cttcacacag	360
ccctccaaga	tgaggcgccg	agtgattgca	cggcctgtgg	gtagctctgt	gcggctcaag	420
tgtgtggcca	gtgggcaccc	acggccagac	atcatgtgga	tgaaggatga	ccagaccttg	480
acgcacttag	aggctagtga	acacagaaag	aagaagtgga	cactgagctt	gaagaacctg	540
aagcctgaag	acagtggcaa	gtacacgtgc	cgtgtatcta	acaaggccgg	tgccatcaac	600
gccacctaca	aagtggatgt	aatccacccc	aaacctccag	ggcctcctat	ggcttcttca	660
tcgtcatcca	caagcctgcc	atggcctgtg	gtgatcgcca	tcccagctgg	tgctgtcttc	720
atcctaggca	ctgtgctgct	ctggctttgc	cagaccaaga	agaagccatg	tgccccagca	780
tctacacttc	ctgtgcctgg	gcatcgctcc	ccaggacat	cccgagaacg	cagtgggtgac	840
aaggacctgc	cctcattggc	tgtgggcata	tgtgaggagc	atggatccgc	catggcccc	900

cagcacatcc	tggcctctgg	ctcaactgct	ggccccaagc	tgtaccccaa	gctatacaca	960
gatgtgcaca	cacacacaca	tacacacacc	tgacttcaca	cgctctcatg	tgaggaggcaa	1020
ggttcatcaa	caccagcatg	tccactatca	gtgctaaata	cagcgaatct	ccaagcactg	1080
tgtcctgagg	taggcatttg	ggggccaagg	caacaggttg	ggagaattga	gaacaatgga	1140
ggaagagtat	cttag					1155

<210> 93
 <211> 384
 <212> PRT
 <213> Mouse

<400> 93

Met	Thr	Arg	Ser	Pro	Ala	Leu	Leu	Leu	Leu	Leu	Leu	Gly	Ala	Leu	Pro	
1				5					10					15		
Ser	Ala	Glu	Ala	Ala	Arg	Gly	Pro	Pro	Arg	Met	Ala	Asp	Lys	Val	Val	
		20						25					30			
Pro	Arg	Gln	Val	Ala	Arg	Leu	Gly	Arg	Thr	Val	Arg	Leu	Gln	Cys	Pro	
		35					40					45				
Val	Glu	Gly	Asp	Pro	Pro	Pro	Leu	Thr	Met	Trp	Thr	Lys	Asp	Gly	Arg	
	50					55					60					
Thr	Ile	His	Ser	Gly	Trp	Ser	Arg	Phe	Arg	Val	Leu	Pro	Gln	Gly	Leu	
65				70					75						80	
Lys	Val	Lys	Glu	Val	Glu	Ala	Glu	Asp	Ala	Gly	Val	Tyr	Val	Cys	Lys	
			85					90						95		
Ala	Thr	Asn	Gly	Phe	Gly	Ser	Leu	Ser	Val	Asn	Tyr	Thr	Leu	Ile	Ile	
		100					105						110			
Met	Ala	Arg	Pro	Arg	Phe	Thr	Gln	Pro	Ser	Lys	Met	Arg	Arg	Arg	Val	
		115					120					125				
Ile	Ala	Arg	Pro	Val	Gly	Ser	Ser	Val	Arg	Leu	Lys	Cys	Val	Ala	Ser	
	130					135					140					
Gly	His	Pro	Arg	Pro	Asp	Ile	Met	Trp	Met	Lys	Asp	Asp	Gln	Thr	Leu	
145				150					155						160	
Thr	His	Leu	Glu	Ala	Ser	Glu	His	Arg	Lys	Lys	Lys	Trp	Thr	Leu	Ser	
			165					170						175		
Leu	Lys	Asn	Leu	Lys	Pro	Glu	Asp	Ser	Gly	Lys	Tyr	Thr	Cys	Arg	Val	
		180					185						190			
Ser	Asn	Lys	Ala	Gly	Ala	Ile	Asn	Ala	Thr	Tyr	Lys	Val	Asp	Val	Ile	
	195					200					205					
His	Pro	Lys	Pro	Pro	Gly	Pro	Pro	Met	Ala	Ser	Ser	Ser	Ser	Ser	Thr	
	210				215						220					
Ser	Leu	Pro	Trp	Pro	Val	Val	Ile	Gly	Ile	Pro	Ala	Gly	Ala	Val	Phe	
225				230					235					240		
Ile	Leu	Gly	Thr	Val	Leu	Leu	Trp	Leu	Cys	Gln	Thr	Lys	Lys	Lys	Pro	
			245					250						255		
Cys	Ala	Pro	Ala	Ser	Thr	Leu	Pro	Val	Pro	Gly	His	Arg	Pro	Pro	Gly	
		260					265					270				
Thr	Ser	Arg	Glu	Arg	Ser	Gly	Asp	Lys	Asp	Leu	Pro	Ser	Leu	Ala	Val	
		275				280						285				
Gly	Ile	Cys	Glu	Glu	His	Gly	Ser	Ala	Met	Ala	Pro	Gln	His	Ile	Leu	
	290				295						300					
Ala	Ser	Gly	Ser	Thr	Ala	Gly	Pro	Lys	Leu	Tyr	Pro	Lys	Leu	Tyr	Thr	
305				310					315					320		
Asp	Val	His	Thr	His	Thr	His	Thr	His	Thr	Cys	Thr	His	Thr	Leu	Ser	
			325					330						335		
Cys	Gly	Gly	Gln	Gly	Ser	Ser	Thr	Pro	Ala	Cys	Pro	Leu	Ser	Val	Leu	
		340					345					350				
Asn	Thr	Ala	Asn	Leu	Gln	Ala	Leu	Cys	Pro	Glu	Val	Gly	Ile	Trp	Gly	

	355		360		365										
Pro	Arg	Gln	Gln	Val	Gly	Arg	Ile	Glu	Asn	Asn	Gly	Gly	Arg	Val	Ser
	370					375					380				

<210> 94
 <211> 1224
 <212> DNA
 <213> Mouse

<400> 94

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cgcactgtgc	ggctacagt	cccagtggag	ggggaccac	caccgttgac	catgtggacc	180
aaagatggcc	gcacaatcca	cagtggctgg	agccgcttcc	gtgtgctgcc	ccagggctctg	240
aaggtgaagg	aggtggaggc	cgaggatgcc	ggtgtttatg	tgtgcaaggc	caccaatggc	300
tttggcagcc	tcagcgtcaa	ctacactctc	atcatcatgg	agcggactcg	ttccaagcct	360
gtgctcacag	ggacacaccc	tgtgaacaca	acggtggact	tcggtgggac	aacgtccttc	420
cagtgaagg	tgcgcagtga	cgtgaagcct	gtgatccagt	ggctgaagcg	ggtggagtac	480
ggctccgagg	gacgccacaa	ctccaccatt	gatgtgggtg	gccagaagtt	tgtgggtgtg	540
cccacgggtg	atgtgtggtc	acggcctgat	ggctcctacc	tcaacaagct	gctcatctct	600
cgggccccgc	aggatgatgc	tggcatgtac	atctgcctag	gtgcaaatac	catgggctac	660
agtttccgta	gcgccttcct	cactgtatta	ccagacccca	aacctccagg	gcctcctatg	720
gcttcttcat	cgatcatccac	aagcctgcc	tggcctgtgg	tgatcggcat	cccagctggt	780
gctgtcttca	tcctaggcac	tgtgctgctc	tggctttgcc	agaccaagaa	gaagccatgt	840
gccccagcat	ctacacttcc	tgtgcctggg	catcgtcccc	cagggacatc	ccgagaacgc	900
agtggtgaca	aggacctgcc	ctcattggct	gtgggcatac	gtgaggagca	tggatccgcc	960
atggcccccc	agcacatcct	ggcctctggc	tcaactgctg	gccccaaagc	gtaccccaag	1020
ctatacacag	atgtgcacac	acacacacat	acacacacct	gactcacac	gctctcatgt	1080
ggagggcaag	gttcatcaac	accagcatgt	ccactatcag	tgctaaatac	agcgaatctc	1140
caagcactgt	gtcctgaggt	aggcatttgg	gggccaaggc	aacaggttgg	gagaattgag	1200
aacaatggag	gaagagtatc	ttag				1224

<210> 95
 <211> 407
 <212> PRT
 <213> Mouse

<400> 95

Met	Thr	Arg	Ser	Pro	Ala	Leu	Leu	Leu	Leu	Leu	Gly	Ala	Leu	Pro
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Ser	Ala	Glu	Ala	Ala	Arg	Gly	Pro	Pro	Arg	Met	Ala	Asp	Lys	Val
			20				25					30		
Pro	Arg	Gln	Val	Ala	Arg	Leu	Gly	Arg	Thr	Val	Arg	Leu	Gln	Cys
			35				40					45		
Val	Glu	Gly	Asp	Pro	Pro	Pro	Leu	Thr	Met	Trp	Thr	Lys	Asp	Gly
			50			55					60			
Thr	Ile	His	Ser	Gly	Trp	Ser	Arg	Phe	Arg	Val	Leu	Pro	Gln	Gly
			70						75					80
Lys	Val	Lys	Glu	Val	Glu	Ala	Glu	Asp	Ala	Gly	Val	Tyr	Val	Cys
			85					90					95	
Ala	Thr	Asn	Gly	Phe	Gly	Ser	Leu	Ser	Val	Asn	Tyr	Thr	Leu	Ile
			100				105					110		
Met	Glu	Arg	Thr	Arg	Ser	Lys	Pro	Val	Leu	Thr	Gly	Thr	His	Pro
			115				120					125		
Asn	Thr	Thr	Val	Asp	Phe	Gly	Gly	Thr	Thr	Ser	Phe	Gln	Cys	Lys
			130			135					140			
Arg	Ser	Asp	Val	Lys	Pro	Val	Ile	Gln	Trp	Leu	Lys	Arg	Val	Glu
														Tyr

145					150					155				160	
Gly	Ser	Glu	Gly	Arg	His	Asn	Ser	Thr	Ile	Asp	Val	Gly	Gly	Gln	Lys
				165					170					175	
Phe	Val	Val	Leu	Pro	Thr	Gly	Asp	Val	Trp	Ser	Arg	Pro	Asp	Gly	Ser
			180					185					190		
Tyr	Leu	Asn	Lys	Leu	Leu	Ile	Ser	Arg	Ala	Arg	Gln	Asp	Asp	Ala	Gly
		195					200					205			
Met	Tyr	Ile	Cys	Leu	Gly	Ala	Asn	Thr	Met	Gly	Tyr	Ser	Phe	Arg	Ser
	210					215					220				
Ala	Phe	Leu	Thr	Val	Leu	Pro	Asp	Pro	Lys	Pro	Pro	Gly	Pro	Pro	Met
225					230					235					240
Ala	Ser	Ser	Ser	Ser	Ser	Thr	Ser	Leu	Pro	Trp	Pro	Val	Val	Ile	Gly
				245				250						255	
Ile	Pro	Ala	Gly	Ala	Val	Phe	Ile	Leu	Gly	Thr	Val	Leu	Leu	Trp	Leu
			260					265					270		
Cys	Gln	Thr	Lys	Lys	Lys	Pro	Cys	Ala	Pro	Ala	Ser	Thr	Leu	Pro	Val
		275					280				285				
Pro	Gly	His	Arg	Pro	Pro	Gly	Thr	Ser	Arg	Glu	Arg	Ser	Gly	Asp	Lys
	290					295					300				
Asp	Leu	Pro	Ser	Leu	Ala	Val	Gly	Ile	Cys	Glu	Glu	His	Gly	Ser	Ala
305					310					315					320
Met	Ala	Pro	Gln	His	Ile	Leu	Ala	Ser	Gly	Ser	Thr	Ala	Gly	Pro	Lys
			325						330					335	
Leu	Tyr	Pro	Lys	Leu	Tyr	Thr	Asp	Val	His	Thr	His	Thr	His	Thr	His
		340						345				350			
Thr	Cys	Thr	His	Thr	Leu	Ser	Cys	Gly	Gly	Gln	Gly	Ser	Ser	Thr	Pro
		355					360					365			
Ala	Cys	Pro	Leu	Ser	Val	Leu	Asn	Thr	Ala	Asn	Leu	Gln	Ala	Leu	Cys
	370					375					380				
Pro	Glu	Val	Gly	Ile	Trp	Gly	Pro	Arg	Gln	Gln	Val	Gly	Arg	Ile	Glu
385					390				395						400
Asn	Asn	Gly	Gly	Arg	Val	Ser									
				405											

<210> 96
 <211> 963
 <212> DNA
 <213> Mouse

<400> 96	
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caggaggacc cagccagcca gcagtgggca cggcctcgct tcacacagcc ctccaagatg	180
aggcgccgag tgattgcacg gcctgtgggt agctctgtgc ggctcaagtg tgtggccagt	240
gggcacccac ggccagacat catgtggatg aaggatgacc agaccttgac gcatctagag	300
gctagtgaac acagaaagaa gaagtggaca ctgagcttga agaacctgaa gcctgaagac	360
agtggcaagt acacgtgccg tgtatctaac aaggccgggtg ccatcaacgc cacctacaaa	420
gtggatgtaa tccaccccaa acctccaggg cctcctatgg cttcttcatc gtcatccaca	480
agcctgccat ggctgtgggt gatcggcatc ccagctgggtg ctgtcttcat cctaggcact	540
gtgctgctct ggctttgcc aaccaagaag aagccatgtg ccccgacatc tacacttcct	600
gtgcctgggc atcgcccc agggacatcc cgagaacgca gtggtgacaa ggacctgccc	660
tcattggctg tgggcatatg tgaggagcat ggatccgcca tggccccca gcacatcctg	720
gcctctggct caactgctgg cccaagctg taccccaagc tatacacaga tgtgcacaca	780
cacacacata cacacacctg cactcacacg ctctcatgtg gagggcaagg ttcataca	840
ccagcatgtc cactatcagt gctaaatata gcgaatctcc aagcactgtg tcctgaggtg	900
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tag	963

<210> 97
 <211> 320
 <212> PRT
 <213> Mouse

<400> 97

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Ser	Ala	Glu	Ala	Ala	Arg	Asp	Asp	Ile	Ser	Pro	Gly	Lys	Glu	Ser	Pro
			20					25					30		
Gly	Pro	Gly	Gly	Ser	Ser	Gly	Gly	Gln	Glu	Asp	Pro	Ala	Ser	Gln	Gln
		35					40					45			
Trp	Ala	Arg	Pro	Arg	Phe	Thr	Gln	Pro	Ser	Lys	Met	Arg	Arg	Arg	Val
	50					55					60				
Ile	Ala	Arg	Pro	Val	Gly	Ser	Ser	Val	Arg	Leu	Lys	Cys	Val	Ala	Ser
65					70					75				80	
Gly	His	Pro	Arg	Pro	Asp	Ile	Met	Trp	Met	Lys	Asp	Asp	Gln	Thr	Leu
				85					90					95	
Thr	His	Leu	Glu	Ala	Ser	Glu	His	Arg	Lys	Lys	Lys	Trp	Thr	Leu	Ser
			100					105					110		
Leu	Lys	Asn	Leu	Lys	Pro	Glu	Asp	Ser	Gly	Lys	Tyr	Thr	Cys	Arg	Val
		115					120					125			
Ser	Asn	Lys	Ala	Gly	Ala	Ile	Asn	Ala	Thr	Tyr	Lys	Val	Asp	Val	Ile
	130					135					140				
His	Pro	Lys	Pro	Pro	Gly	Pro	Pro	Met	Ala	Ser	Ser	Ser	Ser	Ser	Thr
145					150					155					160
Ser	Leu	Pro	Trp	Pro	Val	Val	Ile	Gly	Ile	Pro	Ala	Gly	Ala	Val	Phe
				165					170					175	
Ile	Leu	Gly	Thr	Val	Leu	Leu	Trp	Leu	Cys	Gln	Thr	Lys	Lys	Lys	Pro
			180					185					190		
Cys	Ala	Pro	Ala	Ser	Thr	Leu	Pro	Val	Pro	Gly	His	Arg	Pro	Pro	Gly
		195					200					205			
Thr	Ser	Arg	Glu	Arg	Ser	Gly	Asp	Lys	Asp	Leu	Pro	Ser	Leu	Ala	Val
	210					215					220				
Gly	Ile	Cys	Glu	Glu	His	Gly	Ser	Ala	Met	Ala	Pro	Gln	His	Ile	Leu
225					230					235					240
Ala	Ser	Gly	Ser	Thr	Ala	Gly	Pro	Lys	Leu	Tyr	Pro	Lys	Leu	Tyr	Thr
				245					250					255	
Asp	Val	His	Thr	His	Thr	His	Thr	His	Thr	Cys	Thr	His	Thr	Leu	Ser
			260					265					270		
Cys	Gly	Gly	Gln	Gly	Ser	Ser	Thr	Pro	Ala	Cys	Pro	Leu	Ser	Val	Leu
		275					280					285			
Asn	Thr	Ala	Asn	Leu	Gln	Ala	Leu	Cys	Pro	Glu	Val	Gly	Ile	Trp	Gly
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Pro	Arg	Gln	Gln	Val	Gly	Arg	Ile	Glu	Asn	Asn	Gly	Gly	Arg	Val	Ser
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<210> 98
 <211> 1032
 <212> DNA
 <213> Mouse

<400> 98

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cgccacaact	ccaccattga	tgtgggtggc	cagaagtttg	tgggtgtgcc	cacgggtgat	360
gtgtggtcac	ggcctgatgg	ctcctacctc	aacaagctgc	tcatctctcg	ggcccgccag	420
gatgatgctg	gcatgtacat	ctgcctaggt	gcaaatacca	tgggctacag	tttccgtagc	480
gccttcctca	ctgtattacc	agaccccaaa	cctccagggc	ctcctatggc	ttcttcatcg	540
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ctaggcactg	tgctgctctg	gctttgccag	accaagaaga	agccatgtgc	cccagcatct	660
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gacctgccct	cattggctgt	gggcatatgt	gaggagcatg	gatccgccat	ggccccccag	780
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gtgcacacac	acacacatac	acacacctgc	actcacacgc	tctcatgtgg	agggcaaggt	900
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cctgaggtag	gcatttgggg	gccaaaggcaa	caggttggga	gaattgagaa	caatggagga	1020
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<210> 99

<211> 343

<212> PRT

<213> Mouse

<400> 99

Met	Thr	Arg	Ser	Pro	Ala	Leu	Leu	Leu	Leu	Leu	Gly	Ala	Leu	Pro
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Ser	Ala	Glu	Ala	Ala	Arg	Asp	Asp	Ile	Ser	Pro	Gly	Lys	Glu	Ser
			20				25					30		Pro
Gly	Pro	Gly	Gly	Ser	Ser	Gly	Gly	Gln	Glu	Asp	Pro	Ala	Ser	Gln
		35				40					45			Gln
Trp	Glu	Arg	Thr	Arg	Ser	Lys	Pro	Val	Leu	Thr	Gly	Thr	His	Pro
	50					55					60			Val
Asn	Thr	Thr	Val	Asp	Phe	Gly	Gly	Thr	Thr	Ser	Phe	Gln	Cys	Lys
65				70				75						80
Arg	Ser	Asp	Val	Lys	Pro	Val	Ile	Gln	Trp	Leu	Lys	Arg	Val	Glu
			85					90				95		Tyr
Gly	Ser	Glu	Gly	Arg	His	Asn	Ser	Thr	Ile	Asp	Val	Gly	Gly	Gln
		100					105					110		Lys
Phe	Val	Val	Leu	Pro	Thr	Gly	Asp	Val	Trp	Ser	Arg	Pro	Asp	Gly
		115				120					125			Ser
Tyr	Leu	Asn	Lys	Leu	Leu	Ile	Ser	Arg	Ala	Arg	Gln	Asp	Asp	Ala
	130					135					140			Gly
Met	Tyr	Ile	Cys	Leu	Gly	Ala	Asn	Thr	Met	Gly	Tyr	Ser	Phe	Arg
145				150					155					160
Ala	Phe	Leu	Thr	Val	Leu	Pro	Asp	Pro	Lys	Pro	Pro	Gly	Pro	Pro
			165					170					175	Met
Ala	Ser	Ser	Ser	Ser	Ser	Thr	Ser	Leu	Pro	Trp	Pro	Val	Val	Ile
			180					185				190		Gly
Ile	Pro	Ala	Gly	Ala	Val	Phe	Ile	Leu	Gly	Thr	Val	Leu	Leu	Trp
		195				200					205			Leu
Cys	Gln	Thr	Lys	Lys	Lys	Pro	Cys	Ala	Pro	Ala	Ser	Thr	Leu	Pro
	210					215					220			Val
Pro	Gly	His	Arg	Pro	Pro	Gly	Thr	Ser	Arg	Glu	Arg	Ser	Gly	Asp
225				230					235					Lys
Asp	Leu	Pro	Ser	Leu	Ala	Val	Gly	Ile	Cys	Glu	Glu	His	Gly	Ser
			245					250					255	Ala
Met	Ala	Pro	Gln	His	Ile	Leu	Ala	Ser	Gly	Ser	Thr	Ala	Gly	Pro
		260					265					270		Lys
Leu	Tyr	Pro	Lys	Leu	Tyr	Thr	Asp	Val	His	Thr	His	Thr	His	Thr

	275						280					285							
Thr	Cys	Thr	His	Thr	Leu	Ser	Cys	Gly	Gly	Gln	Gly	Ser	Ser	Thr	Pro				
	290					295					300								
Ala	Cys	Pro	Leu	Ser	Val	Leu	Asn	Thr	Ala	Asn	Leu	Gln	Ala	Leu	Cys				
305					310					315					320				
Pro	Glu	Val	Gly	Ile	Trp	Gly	Pro	Arg	Gln	Gln	Val	Gly	Arg	Ile	Glu				
			325						330					335					
Asn	Asn	Gly	Gly	Arg	Val	Ser													
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<210> 100
 <211> 1236
 <212> DNA
 <213> Mouse

<400> 100

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cctgtgggta	gctctgtgcg	gctcaagtgt	gtggccagtg	ggcaccacg	gccagacatc	180
atgtggatga	aggatgacca	gaccttgacg	catctagagg	ctagtgaaca	cagaaagaag	240
aagtggacac	tgagcttgaa	gaacctgaag	cctgaagaca	gtggcaagta	cacgtgccgt	300
gtatctaaca	aggccggtgc	catcaacgcc	acctacaaag	tggatgtaat	ccagcggact	360
cgttccaagc	ctgtgctcac	agggacacac	cctgtgaaca	caacggtgga	cttcggtggg	420
acaacgtcct	tccagtgcaa	ggtgcgcagt	gacgtgaagc	ctgtgatcca	gtggctgaag	480
cgggtggagt	acggctccga	gggacgccac	aactccacca	ttgatgtggg	tggccagaag	540
tttgtggtgt	tgccacggg	tgatgtgtgg	tcacggcctg	atggctccta	cctcaacaag	600
ctgctcatct	ctcgggcccc	ccaggatgat	gctggcatgt	acatctgcct	aggtgcaa	660
accatgggct	acagtttccg	tagcgccttc	ctcactgtat	taccagacct	caaacctcca	720
gggcctccta	tggcttcttc	atcgtcatcc	acaagcctgc	catggcctgt	ggtgatcggc	780
atcccagctg	gtgctgtctt	catcctaggc	actgtgctgc	tctggctttg	ccagaccaag	840
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tcccagagaac	gcagtgggtga	caaggacctg	ccctcattgg	ctgtgggcat	atgtgaggag	960
catggatccg	ccatggcccc	ccagcacatc	ctggcctctg	gctcaactgc	tggccccaag	1020
ctgtacccca	agctatacac	agatgtgcac	acacacacac	atacacacac	ctgcactcac	1080
acgctctcat	gtggagggca	aggttcatca	acaccagcat	gtccactatc	agtgtctaat	1140
acagcgaatc	tccaagcact	gtgtcctgag	gtaggcattt	gggggccaag	gcaacaggtt	1200
gggagaattg	agaacaatgg	aggaagagta	tcttag			1236

<210> 101
 <211> 411
 <212> PRT
 <213> Mouse

<400> 101

Met	Thr	Arg	Ser	Pro	Ala	Leu	Leu	Leu	Leu	Leu	Gly	Ala	Leu	Pro
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Ser	Ala	Glu	Ala	Ala	Arg	Ala	Arg	Pro	Arg	Phe	Thr	Gln	Pro	Ser
			20				25					30		Lys
Met	Arg	Arg	Arg	Val	Ile	Ala	Arg	Pro	Val	Gly	Ser	Ser	Val	Arg
		35				40					45			Leu
Lys	Cys	Val	Ala	Ser	Gly	His	Pro	Arg	Pro	Asp	Ile	Met	Trp	Met
	50				55					60				Lys
Asp	Asp	Gln	Thr	Leu	Thr	His	Leu	Glu	Ala	Ser	Glu	His	Arg	Lys
65				70					75					80
Lys	Trp	Thr	Leu	Ser	Leu	Lys	Asn	Leu	Lys	Pro	Glu	Asp	Ser	Gly
			85				90					95		Lys
Tyr	Thr	Cys	Arg	Val	Ser	Asn	Lys	Ala	Gly	Ala	Ile	Asn	Ala	Thr

cccaagctat	acacagatgt	gcacacacac	acacatacac	acacctgcac	tcacacgctc	720
tcatgtggag	ggcaagggttc	atcaacacca	gcatgtccac	tatcagtgtc	aaatacagcg	780
aatctccaag	cactgtgtcc	tgaggtaggc	atttgggggc	caaggcaaca	ggttgggaga	840
attgagaaca	atggaggaag	agtatcttag				870

<210> 103
 <211> 289
 <212> PRT
 <213> Mouse

<400> 103

Met	Thr	Arg	Ser	Pro	Ala	Leu	Leu	Leu	Leu	Leu	Leu	Gly	Ala	Leu	Pro
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Ser	Ala	Glu	Ala	Ala	Arg	Gly	Pro	Pro	Arg	Met	Ala	Asp	Lys	Val	Val
			20					25					30		
Pro	Arg	Gln	Val	Ala	Arg	Leu	Gly	Arg	Thr	Val	Arg	Leu	Gln	Cys	Pro
			35				40					45			
Val	Glu	Gly	Asp	Pro	Pro	Pro	Leu	Thr	Met	Trp	Thr	Lys	Asp	Gly	Arg
	50					55					60				
Thr	Ile	His	Ser	Gly	Trp	Ser	Arg	Phe	Arg	Val	Leu	Pro	Gln	Gly	Leu
65					70					75					80
Lys	Val	Lys	Glu	Val	Glu	Ala	Glu	Asp	Ala	Gly	Val	Tyr	Val	Cys	Lys
				85					90					95	
Ala	Thr	Asn	Gly	Phe	Gly	Ser	Leu	Ser	Val	Asn	Tyr	Thr	Leu	Ile	Ile
			100					105					110		
Met	Asp	Pro	Lys	Pro	Pro	Gly	Pro	Pro	Met	Ala	Ser	Ser	Ser	Ser	Ser
		115					120					125			
Thr	Ser	Leu	Pro	Trp	Pro	Val	Val	Ile	Gly	Ile	Pro	Ala	Gly	Ala	Val
	130					135						140			
Phe	Ile	Leu	Gly	Thr	Val	Leu	Leu	Trp	Leu	Cys	Gln	Thr	Lys	Lys	Lys
145					150					155					160
Pro	Cys	Ala	Pro	Ala	Ser	Thr	Leu	Pro	Val	Pro	Gly	His	Arg	Pro	Pro
				165					170					175	
Gly	Thr	Ser	Arg	Glu	Arg	Ser	Gly	Asp	Lys	Asp	Leu	Pro	Ser	Leu	Ala
			180					185					190		
Val	Gly	Ile	Cys	Glu	Glu	His	Gly	Ser	Ala	Met	Ala	Pro	Gln	His	Ile
	195						200						205		
Leu	Ala	Ser	Gly	Ser	Thr	Ala	Gly	Pro	Lys	Leu	Tyr	Pro	Lys	Leu	Tyr
	210					215						220			
Thr	Asp	Val	His	Thr	His	Thr	His	Thr	His	Thr	Cys	Thr	His	Thr	Leu
225					230					235					240
Ser	Cys	Gly	Gly	Gln	Gly	Ser	Ser	Thr	Pro	Ala	Cys	Pro	Leu	Ser	Val
				245					250					255	
Leu	Asn	Thr	Ala	Asn	Leu	Gln	Ala	Leu	Cys	Pro	Glu	Val	Gly	Ile	Trp
			260					265					270		
Gly	Pro	Arg	Gln	Gln	Val	Gly	Arg	Ile	Glu	Asn	Asn	Gly	Gly	Arg	Val
		275					280					285			

Ser

<210> 104
 <211> 678
 <212> DNA
 <213> Mouse

<400> 104

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caggaggacc	cagccagcca	gcagtgggac	cccaaacctc	cagggcctcc	tatggcttct	180
tcatcgtcat	ccacaagcct	gccatggcct	gtggtgatcg	gcacccagc	tggtgctgtc	240
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acagatgtgc	acacacacac	acatacacac	acctgcactc	acacgctctc	atgtggaggg	540
caaggttcat	caacaccagc	atgtccacta	tcagtgtctaa	atacagcgaa	tctccaagca	600
ctgtgtcctg	aggtaggcat	ttggggggcca	aggcaacagg	ttggggagaat	tgagaacaat	660
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<210> 105
 <211> 225
 <212> PRT
 <213> Mouse

<400> 105

Met	Thr	Arg	Ser	Pro	Ala	Leu	Leu	Leu	Leu	Leu	Gly	Ala	Leu	Pro
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Ser	Ala	Glu	Ala	Arg	Asp	Asp	Ile	Ser	Pro	Gly	Lys	Glu	Ser	Pro
		20					25				30			
Gly	Pro	Gly	Gly	Ser	Ser	Gly	Gly	Gln	Glu	Asp	Pro	Ala	Ser	Gln
		35				40					45			
Trp	Asp	Pro	Lys	Pro	Pro	Gly	Pro	Pro	Met	Ala	Ser	Ser	Ser	Ser
	50					55			60					
Thr	Ser	Leu	Pro	Trp	Pro	Val	Val	Ile	Gly	Ile	Pro	Ala	Gly	Ala
65				70				75						80
Phe	Ile	Leu	Gly	Thr	Val	Leu	Leu	Trp	Leu	Cys	Gln	Thr	Lys	Lys
				85				90					95	
Pro	Cys	Ala	Pro	Ala	Ser	Thr	Leu	Pro	Val	Pro	Gly	His	Arg	Pro
			100				105					110		
Gly	Thr	Ser	Arg	Glu	Arg	Ser	Gly	Asp	Lys	Asp	Leu	Pro	Ser	Leu
	115					120					125			Ala
Val	Gly	Ile	Cys	Glu	Glu	His	Gly	Ser	Ala	Met	Ala	Pro	Gln	His
	130					135				140				Ile
Leu	Ala	Ser	Gly	Ser	Thr	Ala	Gly	Pro	Lys	Leu	Tyr	Pro	Lys	Leu
145				150				155						160
Thr	Asp	Val	His	Thr	His	Thr	His	Thr	His	Cys	Thr	His	Thr	Leu
			165				170					175		
Ser	Cys	Gly	Gly	Gln	Gly	Ser	Ser	Thr	Pro	Ala	Cys	Pro	Leu	Ser
		180					185					190		Val
Leu	Asn	Thr	Ala	Asn	Leu	Gln	Ala	Leu	Cys	Pro	Glu	Val	Gly	Ile
	195					200					205			Trp
Gly	Pro	Arg	Gln	Gln	Val	Gly	Arg	Ile	Glu	Asn	Asn	Gly	Gly	Arg
	210				215						220			Val

Ser
 225

<210> 106
 <211> 882
 <212> DNA
 <213> Mouse

<400> 106

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cctgtgggta	gctctgtgcg	gctcaagtgt	gtggccagt	ggcaccacg	gccagacatc	180
atgtggatga	aggatgacca	gaccttgacg	catctagagg	ctagtgaaca	cagaaagaag	240
aagtggacac	tgagcttgaa	gaacctgaag	cctgaagaca	gtggcaagta	cacgtgccgt	300
gtatctaaca	aggccgggtgc	catcaacgcc	acctacaaaag	tgatgtaat	ccaccccaaa	360
cctccagggc	ctcctatggc	ttcttcatcg	tcattccacaa	gcctgccatg	gcctgtggtg	420
atcggcatcc	cagctgggtgc	tgtcttcatc	ctaggcactg	tgctgctctg	gctttgccag	480
accaagaaga	agccatgtgc	cccagcatct	acacttcctg	tgctgggca	tcgtcccca	540
gggacatccc	gagaacgcag	tggtgacaag	gacctgccct	cattggctgt	gggcatatgt	600
gaggagcatg	gatccgccat	ggccccccag	cacatcctgg	cctctggctc	aactgctggc	660
cccaagctgt	acccaagct	atacacagat	gtgcacacac	acacacatac	acacacctgc	720
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ctaaatacag	cgaatctcca	agcactgtgt	cctgaggtag	gcatttgggg	gccaaggcaa	840
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<210> 107

<211> 293

<212> PRT

<213> Mouse

<400> 107

Met	Thr	Arg	Ser	Pro	Ala	Leu	Leu	Leu	Leu	Leu	Gly	Ala	Leu	Pro
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Ser	Ala	Glu	Ala	Arg	Ala	Arg	Pro	Arg	Phe	Thr	Gln	Pro	Ser	Lys
			20				25				30			
Met	Arg	Arg	Arg	Val	Ile	Ala	Arg	Pro	Val	Gly	Ser	Ser	Val	Arg
			35				40				45			
Lys	Cys	Val	Ala	Ser	Gly	His	Pro	Arg	Pro	Asp	Ile	Met	Trp	Met
	50					55				60				
Asp	Asp	Gln	Thr	Leu	Thr	His	Leu	Glu	Ala	Ser	Glu	His	Arg	Lys
65					70				75					80
Lys	Trp	Thr	Leu	Ser	Leu	Lys	Asn	Leu	Lys	Pro	Glu	Asp	Ser	Gly
			85					90					95	
Tyr	Thr	Cys	Arg	Val	Ser	Asn	Lys	Ala	Gly	Ala	Ile	Asn	Ala	Thr
			100					105				110		
Lys	Val	Asp	Val	Ile	His	Pro	Lys	Pro	Pro	Gly	Pro	Pro	Met	Ala
	115						120				125			
Ser	Ser	Ser	Ser	Thr	Ser	Leu	Pro	Trp	Pro	Val	Val	Ile	Gly	Ile
	130					135					140			
Ala	Gly	Ala	Val	Phe	Ile	Leu	Gly	Thr	Val	Leu	Leu	Trp	Leu	Cys
145					150				155					160
Thr	Lys	Lys	Lys	Pro	Cys	Ala	Pro	Ala	Ser	Thr	Leu	Pro	Val	Pro
			165					170					175	
His	Arg	Pro	Pro	Gly	Thr	Ser	Arg	Glu	Arg	Ser	Gly	Asp	Lys	Asp
			180					185				190		
Pro	Ser	Leu	Ala	Val	Gly	Ile	Cys	Glu	Glu	His	Gly	Ser	Ala	Met
	195						200					205		
Pro	Gln	His	Ile	Leu	Ala	Ser	Gly	Ser	Thr	Ala	Gly	Pro	Lys	Leu
	210					215					220			
Pro	Lys	Leu	Tyr	Thr	Asp	Val	His	Thr	His	Thr	His	Thr	His	Thr
225					230				235					240
Thr	His	Thr	Leu	Ser	Cys	Gly	Gly	Gln	Gly	Ser	Ser	Thr	Pro	Ala
			245					250					255	
Pro	Leu	Ser	Val	Leu	Asn	Thr	Ala	Asn	Leu	Gln	Ala	Leu	Cys	Pro
	260							265				270		
Val	Gly	Ile	Trp	Gly	Pro	Arg	Gln	Gln	Val	Gly	Arg	Ile	Glu	Asn
	275					280					285			
Gly	Gly	Arg	Val	Ser										

290

<210> 108
<211> 951
<212> DNA
<213> Mouse

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<400> 108
atgacgcgga gccccgcgct gctgctgctg ctattggggg ccctcccgtc ggctgaggcg      60
gcgcgagagc ggactcgttc caagcctgtg ctcacaggga cacaccctgt gaacacaacg      120
gtggacttcg gtgggacaac gtccttcagg tgcaagggtg gcagtgcagt gaagcctgtg      180
atccagtggc tgaagcgggt ggagtacggc tccgaggggac gccacaactc caccattgat      240
gtgggtggcc agaagtttgt ggtgttgccc acgggtgatg tgtggtcacg gcctgatggc      300
tcctacctca acaagctgct catctctcgg gcccgccagg atgatgctgg catgtacatc      360
tgcctaggtg caaataccat gggctacagt ttccgtagcg ccttcctcac tgtattacca      420
gaccccaaac ctccagggcc tcctatggct tcttcatcgt catccacaag cctgccatgg      480
cctgtggtga tcggcatccc agctggtgct gtcttcatcc taggcactgt gctgctctgg      540
ctttgccaga ccaagaagaa gccatgtgcc ccagcatcta cacttcctgt gcctgggcat      600
cgtcccccag ggacatcccg agaacgcagt ggtgacaagg acctgccctc attggctgtg      660
ggcatatgtg aggagcatgg atccgccatg gccccccagc acatcctggc ctctgggtca      720
actgctggcc ccaagctgta cccaagcta tacacagatg tgcacacaca cacacataca      780
cacacctgca ctcacacgct ctcatgtgga gggcaagggt catcaacacc agcatgtcca      840
ctatcagtgc taaatacagc gaatctccaa gcactgtgtc ctgaggtagg catttggggg      900
ccaaggcaac aggttgggag aattgagaac aatggaggaa gagtatctta g      951

```

<210> 109
<211> 316
<212> PRT
<213> Mouse

```

<400> 109
Met Thr Arg Ser Pro Ala Leu Leu Leu Leu Leu Leu Gly Ala Leu Pro
 1          5          10          15
Ser Ala Glu Ala Ala Arg Glu Arg Thr Arg Ser Lys Pro Val Leu Thr
          20          25          30
Gly Thr His Pro Val Asn Thr Thr Val Asp Phe Gly Gly Thr Thr Ser
          35          40          45
Phe Gln Cys Lys Val Arg Ser Asp Val Lys Pro Val Ile Gln Trp Leu

          50          55          60
Lys Arg Val Glu Tyr Gly Ser Glu Gly Arg His Asn Ser Thr Ile Asp
65          70          75          80
Val Gly Gly Gln Lys Phe Val Val Leu Pro Thr Gly Asp Val Trp Ser
          85          90          95
Arg Pro Asp Gly Ser Tyr Leu Asn Lys Leu Leu Ile Ser Arg Ala Arg
          100          105          110
Gln Asp Asp Ala Gly Met Tyr Ile Cys Leu Gly Ala Asn Thr Met Gly
          115          120          125
Tyr Ser Phe Arg Ser Ala Phe Leu Thr Val Leu Pro Asp Pro Lys Pro
          130          135          140
Pro Gly Pro Pro Met Ala Ser Ser Ser Ser Ser Thr Ser Leu Pro Trp
145          150          155          160
Pro Val Val Ile Gly Ile Pro Ala Gly Ala Val Phe Ile Leu Gly Thr
          165          170          175
Val Leu Leu Trp Leu Cys Gln Thr Lys Lys Lys Pro Cys Ala Pro Ala
          180          185          190
Ser Thr Leu Pro Val Pro Gly His Arg Pro Pro Gly Thr Ser Arg Glu

```

195	200	205
Arg Ser Gly Asp Lys Asp	Leu Pro Ser Leu Ala Val	Gly Ile Cys Glu
210	215	220
Glu His Gly Ser Ala Met	Ala Pro Gln His Ile	Leu Ala Ser Gly Ser
225	230	235
Thr Ala Gly Pro Lys Leu	Tyr Pro Lys Leu Tyr	Thr Asp Val His Thr
245	250	255
His Thr His Thr His Thr	Cys Thr His Thr Leu	Ser Cys Gly Gly Gln
260	265	270
Gly Ser Ser Thr Pro Ala	Cys Pro Leu Ser Val	Leu Asn Thr Ala Asn
275	280	285
Leu Gln Ala Leu Cys Pro	Glu Val Gly Ile Trp	Gly Pro Arg Gln Gln
290	295	300
Val Gly Arg Ile Glu Asn	Asn Gly Gly Arg Val	Ser
305	310	315

<210> 110
 <211> 597
 <212> DNA
 <213> Mouse

<400> 110	
atgacgcgga gccccgcgct gctgctgctg ctattggggg ccctcccgtc ggctgaggcg	60
gcgcgagacc ccaaacctcc agggcctcct atggcttctt catcgtcatc cacaagcctg	120
ccatggcctg tggatgatcg catcccagct ggtgctgtct tcatcctagg cactgtgctg	180
ctctggcttt gccagaccaa gaagaagcca tgtgccccag catctacact tcctgtgcct	240
gggcatcgct ccccaggac atcccagaaa cgcatgggtg acaaggacct gccctcattg	300
gctgtgggca tatgtgagga gcatggatcc gccatggccc cccagcacat cctggcctct	360
ggctcaactg ctggcccaaa gctgtacccc aagctataca cagatgtgca cacacacaca	420
catacacaca cctgcactca cacgctctca tgtggagggc aaggttcac aacaccagca	480
tgtccactat cagtgtctaaa tacagcgaat ctccaagcac tgtgtcctga ggtaggcatt	540
tgggggcca ggcaacaggt tgggagaatt gagaacaatg gaggaagagt atcttag	597

<210> 111
 <211> 198
 <212> PRT

<213> Mouse

<400> 111
Met Thr Arg Ser Pro Ala Leu Leu Leu Leu Leu Leu Gly Ala Leu Pro
1 5 10 15
Ser Ala Glu Ala Ala Arg Asp Pro Lys Pro Pro Gly Pro Pro Met Ala
20 25 30
Ser Ser Ser Ser Ser Thr Ser Leu Pro Trp Pro Val Val Ile Gly Ile
35 40 45
Pro Ala Gly Ala Val Phe Ile Leu Gly Thr Val Leu Leu Trp Leu Cys
50 55 60
Gln Thr Lys Lys Lys Pro Cys Ala Pro Ala Ser Thr Leu Pro Val Pro
65 70 75 80
Gly His Arg Pro Pro Gly Thr Ser Arg Glu Arg Ser Gly Asp Lys Asp
85 90 95
Leu Pro Ser Leu Ala Val Gly Ile Cys Glu Glu His Gly Ser Ala Met
100 105 110
Ala Pro Gln His Ile Leu Ala Ser Gly Ser Thr Ala Gly Pro Lys Leu
115 120 125
Tyr Pro Lys Leu Tyr Thr Asp Val His Thr His Thr His Thr His Thr

1				5					10					15		
Ser	Ala	Glu	Ala	Ala	Arg	Gly	Pro	Pro	Arg	Met	Ala	Asp	Lys	Val	Val	
			20					25					30			
Pro	Arg	Gln	Val	Ala	Arg	Leu	Gly	Arg	Thr	Val	Arg	Leu	Gln	Cys	Pro	
		35					40					45				
Val	Glu	Gly	Asp	Pro	Pro	Pro	Leu	Thr	Met	Trp	Thr	Lys	Asp	Gly	Arg	
	50					55					60					
Thr	Ile	His	Ser	Gly	Trp	Ser	Arg	Phe	Arg	Val	Leu	Pro	Gln	Gly	Leu	
65					70				75						80	
Lys	Val	Lys	Glu	Val	Glu	Ala	Glu	Asp	Ala	Gly	Val	Tyr	Val	Cys	Lys	
			85					90						95		
Ala	Thr	Asn	Gly	Phe	Gly	Ser	Leu	Ser	Val	Asn	Tyr	Thr	Leu	Ile	Ile	
		100						105					110			
Met	Asp	Asp	Ile	Ser	Pro	Gly	Lys	Glu	Ser	Pro	Gly	Pro	Gly	Gly	Ser	
		115					120					125				

Ser	Gly	Gly	Gln	Glu	Asp	Pro	Ala	Ser	Gln	Gln	Trp	Ala	Arg	Pro	Arg	
	130					135					140					
Phe	Thr	Gln	Pro	Ser	Lys	Met	Arg	Arg	Arg	Val	Ile	Ala	Arg	Pro	Val	
145					150					155					160	
Gly	Ser	Ser	Val	Arg	Leu	Lys	Cys	Val	Ala	Ser	Gly	His	Pro	Arg	Pro	
			165					170						175		
Asp	Ile	Met	Trp	Met	Lys	Asp	Asp	Gln	Thr	Leu	Thr	His	Leu	Glu	Ala	
		180						185					190			
Ser	Glu	His	Arg	Lys	Lys	Lys	Trp	Thr	Leu	Ser	Leu	Lys	Asn	Leu	Lys	
	195						200					205				
Pro	Glu	Asp	Ser	Gly	Lys	Tyr	Thr	Cys	Arg	Val	Ser	Asn	Lys	Ala	Gly	
	210					215					220					
Ala	Ile	Asn	Ala	Thr	Tyr	Lys	Val	Asp	Val	Ile						
225					230					235						

<210> 116
 <211> 775
 <212> DNA
 <213> Mouse

<400> 116

atgacgcgga	gccccgcgct	gctgctgctg	ctattggggg	ccctcccgtc	ggctgaggcg	60
gcgcgaggac	ccccagaat	ggcagacaaa	gtggtcccac	ggcaggtggc	ccgcctgggc	120
cgcactgtgc	ggctacagt	cccagtggag	ggggaccac	caccgttgac	catgtggacc	180
aaagatggcc	gcacaatcca	cagtggctgg	agccgcttcc	gtgtgctgcc	ccagggtctg	240
aaggtgaagg	aggtggaggc	cgaggatgcc	ggtgtttatg	tgtgcaaggc	caccaatggc	300
tttggcagcc	tcagcgtcaa	ctacactctc	atcatcatgg	atgatattag	tccagggaag	360
gagagccctg	ggccaggtgg	ttcttcgggg	ggccaggagg	acccagccag	ccagcagtgg	420
gagcggactc	gttccaagcc	tgtgctcaca	gggacacacc	ctgtgaacac	aacggtggac	480
ttcggtggga	caacgtcctt	ccagtgcaag	gtgcgcagtg	acgtgaagcc	tgtgatccag	540
tggctgaagc	gggtggagta	cggctccgag	ggacgccaca	actccaccat	tgatgtgggt	600
ggccagaagt	ttgtggtgtt	gcccacgggt	gatgtgtggt	cacggcctga	tggctcctac	660
ctcaacaagc	tgctcatctc	tcgggcccgc	caggatgatg	ctggcatgta	catctgccta	720
ggtgcaaata	ccatgggcta	cagtttccgt	agcgccttcc	tcactgtatt	accag	775

<210> 117
 <211> 258
 <212> PRT
 <213> Mouse

<400> 117

Met	Thr	Arg	Ser	Pro	Ala	Leu	Leu	Leu	Leu	Leu	Leu	Gly	Ala	Leu	Pro
1				5					10					15	
Ser	Ala	Glu	Ala	Arg	Gly	Pro	Pro	Arg	Met	Ala	Asp	Lys	Val	Val	
		20				25					30				
Pro	Arg	Gln	Val	Ala	Arg	Leu	Gly	Arg	Thr	Val	Arg	Leu	Gln	Cys	Pro
		35				40					45				
Val	Glu	Gly	Asp	Pro	Pro	Pro	Leu	Thr	Met	Trp	Thr	Lys	Asp	Gly	Arg
	50				55					60					
Thr	Ile	His	Ser	Gly	Trp	Ser	Arg	Phe	Arg	Val	Leu	Pro	Gln	Gly	Leu
65				70					75						80
Lys	Val	Lys	Glu	Val	Glu	Ala	Glu	Asp	Ala	Gly	Val	Tyr	Val	Cys	Lys
			85					90						95	
Ala	Thr	Asn	Gly	Phe	Gly	Ser	Leu	Ser	Val	Asn	Tyr	Thr	Leu	Ile	Ile
		100						105					110		
Met	Asp	Asp	Ile	Ser	Pro	Gly	Lys	Glu	Ser	Pro	Gly	Pro	Gly	Gly	Ser
	115					120					125				
Ser	Gly	Gly	Gln	Glu	Asp	Pro	Ala	Ser	Gln	Gln	Trp	Glu	Arg	Thr	Arg
	130					135					140				
Ser	Lys	Pro	Val	Leu	Thr	Gly	Thr	His	Pro	Val	Asn	Thr	Thr	Val	Asp
145					150					155					160
Phe	Gly	Gly	Thr	Thr	Ser	Phe	Gln	Cys	Lys	Val	Arg	Ser	Asp	Val	Lys
			165					170						175	
Pro	Val	Ile	Gln	Trp	Leu	Lys	Arg	Val	Glu	Tyr	Gly	Ser	Glu	Gly	Arg
		180						185					190		
His	Asn	Ser	Thr	Ile	Asp	Val	Gly	Gly	Gln	Lys	Phe	Val	Val	Leu	Pro
	195						200					205			
Thr	Gly	Asp	Val	Trp	Ser	Arg	Pro	Asp	Gly	Ser	Tyr	Leu	Asn	Lys	Leu
	210					215					220				
Leu	Ile	Ser	Arg	Ala	Arg	Gln	Asp	Asp	Ala	Gly	Met	Tyr	Ile	Cys	Leu
225					230					235					240
Gly	Ala	Asn	Thr	Met	Gly	Tyr	Ser	Phe	Arg	Ser	Ala	Phe	Leu	Thr	Val
			245					250					255		

Leu Pro

<210> 118
 <211> 979
 <212> DNA
 <213> Mouse

<400> 118					
atgacgcgga	gccccgcgct	gctgctgctg	ctattggggg	ccctcccgtc	ggctgaggcg 60
gcgcgaggac	ccccagaat	ggcagacaaa	gtgggtcccac	ggcaggtggc	ccgcctgggc 120
cgcactgtgc	ggctacagt	cccagtggag	ggggaccac	caccgttgac	catgtggacc 180
aaagatggcc	gcacaatcca	cagtggctgg	agccgcttcc	gtgtgctgcc	ccagggctctg 240
aaggtgaagg	aggtggaggc	cgaggatgcc	ggtgtttatg	tgtgcaaggc	caccaatggc 300
tttggcagcc	tcagcgtcaa	ctacactctc	atcatcatgg	cacggcctcg	cttcacacag 360
ccctccaaga	tgaggcgccg	agtgattgca	cggcctgtgg	gtagctctgt	gcggctcaag 420
tgtgtggcca	gtgggcaccc	acggccagac	atcatgtgga	tgaaggatga	ccagaccttg 480
acgcatctag	aggctagtga	acacagaaag	aagaagtgga	cactgagctt	gaagaacctg 540
aagcctgaag	acagtggcaa	gtacacgtgc	cgtgtatcta	acaaggccgg	tgccatcaac 600
gccacctaca	aagtggatgt	aatccagcgg	actcgttcca	agcctgtgct	cacagggaca 660
caccctgtga	acacaacgg	ggacttcgg	gggacaacgt	ccttcagtg	caaggtgcgc 720
agtgcagtga	agcctgtgat	ccagtggctg	aagcgggtgg	agtacggctc	cgagggacgc 780
cacaactcca	ccattgatgt	gggtggccag	aagtttgtgg	tggtgcccac	gggtgatgtg 840
tggtcacggc	ctgatggctc	ctacctcaac	aagctgctca	tctctcgggc	ccgccaggat 900

gatgctggca tgtacatctg cctaggtgca aataccatgg gctacagttt ccgtagcgcc
 ttcctcactg tattaccag

960
 979

<210> 119
 <211> 326
 <212> PRT
 <213> Mouse

<400> 119
 Met Thr Arg Ser Pro Ala Leu Leu Leu Leu Leu Leu Gly Ala Leu Pro
 1 5 10 15
 Ser Ala Glu Ala Ala Arg Gly Pro Pro Arg Met Ala Asp Lys Val Val
 20 25 30
 Pro Arg Gln Val Ala Arg Leu Gly Arg Thr Val Arg Leu Gln Cys Pro
 35 40 45
 Val Glu Gly Asp Pro Pro Pro Leu Thr Met Trp Thr Lys Asp Gly Arg
 50 55 60
 Thr Ile His Ser Gly Trp Ser Arg Phe Arg Val Leu Pro Gln Gly Leu
 65 70 75 80
 Lys Val Lys Glu Val Glu Ala Glu Asp Ala Gly Val Tyr Val Cys Lys
 85 90 95
 Ala Thr Asn Gly Phe Gly Ser Leu Ser Val Asn Tyr Thr Leu Ile Ile
 100 105 110
 Met Ala Arg Pro Arg Phe Thr Gln Pro Ser Lys Met Arg Arg Arg Val
 115 120 125
 Ile Ala Arg Pro Val Gly Ser Ser Val Arg Leu Lys Cys Val Ala Ser
 130 135 140
 Gly His Pro Arg Pro Asp Ile Met Trp Met Lys Asp Asp Gln Thr Leu
 145 150 155 160
 Thr His Leu Glu Ala Ser Glu His Arg Lys Lys Lys Trp Thr Leu Ser
 165 170 175
 Leu Lys Asn Leu Lys Pro Glu Asp Ser Gly Lys Tyr Thr Cys Arg Val
 180 185 190
 Ser Asn Lys Ala Gly Ala Ile Asn Ala Thr Tyr Lys Val Asp Val Ile
 195 200 205
 Gln Arg Thr Arg Ser Lys Pro Val Leu Thr Gly Thr His Pro Val Asn
 210 215 220
 Thr Thr Val Asp Phe Gly Gly Thr Thr Ser Phe Gln Cys Lys Val Arg
 225 230 235 240
 Ser Asp Val Lys Pro Val Ile Gln Trp Leu Lys Arg Val Glu Tyr Gly
 245 250 255
 Ser Glu Gly Arg His Asn Ser Thr Ile Asp Val Gly Gly Gln Lys Phe
 260 265 270
 Val Val Leu Pro Thr Gly Asp Val Trp Ser Arg Pro Asp Gly Ser Tyr
 275 280 285
 Leu Asn Lys Leu Leu Ile Ser Arg Ala Arg Gln Asp Asp Ala Gly Met
 290 295 300
 Tyr Ile Cys Leu Gly Ala Asn Thr Met Gly Tyr Ser Phe Arg Ser Ala
 305 310 315 320
 Phe Leu Thr Val Leu Pro
 325

<210> 120
 <211> 787
 <212> DNA
 <213> Mouse

```

<400> 120
atgacgcgga gccccgcgct gctgctgctg ctattggggg ccctcccgtc ggctgaggcg      60
gcgcgagatg atattagtcc aggggaaggag agccctgggc caggtgggtc ttcggggggc      120
caggaggacc cagccagcca gcagtgggca cggcctcgct tcacacagcc ctccaagatg      180
aggcgccgag tgattgcacg gcctgtgggt agctctgtgc ggctcaagtg tgtggccagt      240
gggcacccac ggccagacat catgtggatg aaggatgacc agaccttgac gcatctagag      300
gctagtgaac acagaaagaa gaagtggaca ctgagcttga agaacctgaa gcctgaagac      360
agtggcaagt acacgtgccg tgtatctaac aaggccggtg ccatcaacgc cacctacaaa      420
gtggatgtaa tccagcggac tcgttccaag cctgtgctca cagggacaca ccctgtgaac      480
acaacggtgg acttcggtgg gacaacgtcc ttccagtgc aagtgcgcgag tgacgtgaag      540
cctgtgatcc agtggctgaa gcgggtggag tacggctccg agggacgcca caactccacc      600
attgatgtgg gtggccagaa gtttgtgggt ttgccacgg gtgatgtgtg gtcacggcct      660
gatggctcct acctcaacaa gctgctcatc tctcggggcc gccaggatga tgctggcatg      720
tacatctgcc taggtgcaaa taccatgggc tacagtttcc gtagcgcctt cctcactgta      780
ttaccag                                         787

```

```

<210> 121
<211> 262
<212> PRT
<213> Mouse

```

```

<400> 121
Met Thr Arg Ser Pro Ala Leu Leu Leu Leu Leu Leu Gly Ala Leu Pro
 1          5          10          15
Ser Ala Glu Ala Ala Arg Asp Asp Ile Ser Pro Gly Lys Glu Ser Pro
          20          25          30
Gly Pro Gly Gly Ser Ser Gly Gly Gln Glu Asp Pro Ala Ser Gln Gln
          35          40          45
Trp Ala Arg Pro Arg Phe Thr Gln Pro Ser Lys Met Arg Arg Arg Val
          50          55          60
Ile Ala Arg Pro Val Gly Ser Ser Val Arg Leu Lys Cys Val Ala Ser
65          70          75          80
Gly His Pro Arg Pro Asp Ile Met Trp Met Lys Asp Asp Gln Thr Leu
          85          90          95
Thr His Leu Glu Ala Ser Glu His Arg Lys Lys Lys Trp Thr Leu Ser
          100          105          110
Leu Lys Asn Leu Lys Pro Glu Asp Ser Gly Lys Tyr Thr Cys Arg Val
          115          120          125
Ser Asn Lys Ala Gly Ala Ile Asn Ala Thr Tyr Lys Val Asp Val Ile
          130          135          140
Gln Arg Thr Arg Ser Lys Pro Val Leu Thr Gly Thr His Pro Val Asn
145          150          155          160
Thr Thr Val Asp Phe Gly Gly Thr Thr Ser Phe Gln Cys Lys Val Arg
          165          170          175
Ser Asp Val Lys Pro Val Ile Gln Trp Leu Lys Arg Val Glu Tyr Gly
          180          185          190
Ser Glu Gly Arg His Asn Ser Thr Ile Asp Val Gly Gly Gln Lys Phe
          195          200          205
Val Val Leu Pro Thr Gly Asp Val Trp Ser Arg Pro Asp Gly Ser Tyr
          210          215          220
Leu Asn Lys Leu Leu Ile Ser Arg Ala Arg Gln Asp Asp Ala Gly Met
225          230          235          240
Tyr Ile Cys Leu Gly Ala Asn Thr Met Gly Tyr Ser Phe Arg Ser Ala
          245          250          255
Phe Leu Thr Val Leu Pro
          260

```


<210> 122
 <211> 421
 <212> DNA
 <213> Mouse

```
<400> 122
atgacgcgga gccccgcgct gctgctgctg ctattggggg ccctcccgtc ggctgaggcg      60
gcgcgaggac ccccaagaat ggcagacaaa gtggtcccac ggcagggtggc ccgcctgggg      120
cgactgtgc  ggctacagtg cccagtggag ggggaccac caccgttgac catgtggacc      180
aaagatggcc gcacaatcca cagtggctgg agccgcttcc gtgtgctgcc ccagggtctg      240
aaggtgaagg aggtggaggc cgaggatgcc ggtgtttatg tgtgcaaggc caccaatggc      300
tttggcagcc tcagcgtcaa ctacactctc atcatcatgg atgatattag tccagggaag      360
gagagccctg ggccagggtg ttcttcgggg ggccaggagg acccagccag ccagcagtgg      420
g                                                                421
```

<210> 123
 <211> 140
 <212> PRT
 <213> Mouse

```
<400> 123
Met Thr Arg Ser Pro Ala Leu Leu Leu Leu Leu Leu Gly Ala Leu Pro
 1              5              10              15
Ser Ala Glu Ala Ala Arg Gly Pro Pro Arg Met Ala Asp Lys Val Val
      20              25              30
Pro Arg Gln Val Ala Arg Leu Gly Arg Thr Val Arg Leu Gln Cys Pro
      35              40              45
Val Glu Gly Asp Pro Pro Pro Leu Thr Met Trp Thr Lys Asp Gly Arg
      50              55              60
Thr Ile His Ser Gly Trp Ser Arg Phe Arg Val Leu Pro Gln Gly Leu
      65              70              75              80
Lys Val Lys Glu Val Glu Ala Glu Asp Ala Gly Val Tyr Val Cys Lys
      85              90              95
Ala Thr Asn Gly Phe Gly Ser Leu Ser Val Asn Tyr Thr Leu Ile Ile
      100             105             110
Met Asp Asp Ile Ser Pro Gly Lys Glu Ser Pro Gly Pro Gly Gly Ser
      115             120             125
Ser Gly Gly Gln Glu Asp Pro Ala Ser Gln Gln Trp
      130             135             140
```

<210> 124
 <211> 625
 <212> DNA
 <213> Mouse

```
<400> 124
atgacgcgga gccccgcgct gctgctgctg ctattggggg ccctcccgtc ggctgaggcg      60
gcgcgaggac ccccaagaat ggcagacaaa gtggtcccac ggcagggtggc ccgcctgggg      120
cgactgtgc  ggctacagtg cccagtggag ggggaccac caccgttgac catgtggacc      180
aaagatggcc gcacaatcca cagtggctgg agccgcttcc gtgtgctgcc ccagggtctg      240
aaggtgaagg aggtggaggc cgaggatgcc ggtgtttatg tgtgcaaggc caccaatggc      300
tttggcagcc tcagcgtcaa ctacactctc atcatcatgg cacggcctcg cttcacacag      360
ccctccaaga tgaggcgccg agtgattgca cggcctgtgg gtagctctgt gcggctcaag      420
tgtgtggcca gtgggcaccc acggccagac atcatgtgga tgaaggatga ccagaccttg      480
acgcatctag aggctagtga acacagaaaag aagaagtgga cactgagctt gaagaacctg      540
aagcctgaag acagtggcaa gtacacgtgc cgtgtatcta acaaggccgg tgccatcaac      600
```

gccacctaca aagtggatgt aatcc

625

<210> 125
<211> 208
<212> PRT
<213> Mouse

<400> 125
Met Thr Arg Ser Pro Ala Leu Leu Leu Leu Leu Leu Gly Ala Leu Pro
1 5 10 15
Ser Ala Glu Ala Ala Arg Gly Pro Pro Arg Met Ala Asp Lys Val Val
20 25 30
Pro Arg Gln Val Ala Arg Leu Gly Arg Thr Val Arg Leu Gln Cys Pro
35 40 45
Val Glu Gly Asp Pro Pro Pro Leu Thr Met Trp Thr Lys Asp Gly Arg
50 55 60
Thr Ile His Ser Gly Trp Ser Arg Phe Arg Val Leu Pro Gln Gly Leu
65 70 75 80
Lys Val Lys Glu Val Glu Ala Glu Asp Ala Gly Val Tyr Val Cys Lys
85 90 95
Ala Thr Asn Gly Phe Gly Ser Leu Ser Val Asn Tyr Thr Leu Ile Ile
100 105 110
Met Ala Arg Pro Arg Phe Thr Gln Pro Ser Lys Met Arg Arg Arg Val
115 120 125
Ile Ala Arg Pro Val Gly Ser Ser Val Arg Leu Lys Cys Val Ala Ser
130 135 140
Gly His Pro Arg Pro Asp Ile Met Trp Met Lys Asp Asp Gln Thr Leu
145 150 155 160
Thr His Leu Glu Ala Ser Glu His Arg Lys Lys Lys Trp Thr Leu Ser
165 170 175
Leu Lys Asn Leu Lys Pro Glu Asp Ser Gly Lys Tyr Thr Cys Arg Val
180 185 190
Ser Asn Lys Ala Gly Ala Ile Asn Ala Thr Tyr Lys Val Asp Val Ile
195 200 205

<210> 126
<211> 694
<212> DNA
<213> Mouse

<400> 126
atgacgcgga gccccgcgct gctgctgctg ctattggggg cctcccgcgc ggctgaggcg 60
gcgcgaggac ccccaagaat ggcagacaaa gtgggtccac ggcaggtggc ccgcctgggc 120
cgactgtgc ggctacagtg ccagtgagg ggggaccac caccgttgac catgtggacc 180
aaagatggcc gcacaatcca cagtggctgg agccgcttcc gtgtgctgcc ccagggctctg 240
aaggtgaagg aggtggaggc cgaggatgcc ggtgtttatg tgtgcaaggc caccaatggc 300
tttggcagcc tcagcgtcaa ctacactctc atcatcatgg agcggactcg ttccaagcct 360
gtgctcacag ggacacaccc tgtgaacaca acggtggact tcggtgggac aacgtccttc 420
cagtgaagg tgccgagtga cgtgaagcct gtgatccagt ggctgaagcg ggtggagtac 480
ggctccgagg gacgccacaa ctccaccatt gatgtgggtg gccagaagtt tgtgggtgtg 540
cccacgggtg atgtgtggtc acggcctgat ggctcctacc tcaacaagct gctcatctct 600
cgggcccgcc aggatgatgc tggcatgtac atctgcctag gtgcaaatac catgggctac 660
agtttccgta gcgccttcct cactgtatta ccag 694

<210> 127
<211> 231
<212> PRT

<213> Mouse

<400> 127

```
Met Thr Arg Ser Pro Ala Leu Leu Leu Leu Leu Leu Gly Ala Leu Pro
 1              5              10              15
Ser Ala Glu Ala Arg Gly Pro Pro Arg Met Ala Asp Lys Val Val
      20              25              30
Pro Arg Gln Val Ala Arg Leu Gly Arg Thr Val Arg Leu Gln Cys Pro
      35              40              45
Val Glu Gly Asp Pro Pro Pro Leu Thr Met Trp Thr Lys Asp Gly Arg
      50              55              60
Thr Ile His Ser Gly Trp Ser Arg Phe Arg Val Leu Pro Gln Gly Leu
65              70              75              80
Lys Val Lys Glu Val Glu Ala Glu Asp Ala Gly Val Tyr Val Cys Lys
      85              90              95
Ala Thr Asn Gly Phe Gly Ser Leu Ser Val Asn Tyr Thr Leu Ile Ile
      100              105              110
Met Glu Arg Thr Arg Ser Lys Pro Val Leu Thr Gly Thr His Pro Val
      115              120              125
Asn Thr Thr Val Asp Phe Gly Gly Thr Thr Ser Phe Gln Cys Lys Val
      130              135              140
Arg Ser Asp Val Lys Pro Val Ile Gln Trp Leu Lys Arg Val Glu Tyr
145              150              155              160
Gly Ser Glu Gly Arg His Asn Ser Thr Ile Asp Val Gly Gly Gln Lys
      165              170              175
Phe Val Val Leu Pro Thr Gly Asp Val Trp Ser Arg Pro Asp Gly Ser
      180              185              190
Tyr Leu Asn Lys Leu Leu Ile Ser Arg Ala Arg Gln Asp Asp Ala Gly
      195              200              205
Met Tyr Ile Cys Leu Gly Ala Asn Thr Met Gly Tyr Ser Phe Arg Ser
      210              215              220
Ala Phe Leu Thr Val Leu Pro
225              230
```

<210> 128

<211> 433

<212> DNA

<213> Mouse

<400> 128

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atgacgcgga gccccgcgct gctgctgctg ctattggggg ccctcccgtc ggctgaggcg      60
gcgcgagatg atattagtcc aggggaaggag agccctgggc caggtgggtc ttcggggggc      120
caggaggacc cagccagcca gcagtgggca cggcctcgct tcacacagcc ctccaagatg      180
aggcgccgag tgattgcacg gcctgtgggt agctctgtgc ggctcaagtg tgtggccagt      240
gggcacccac ggccagacat catgtggatg aaggatgacc agaccttgac gcatctagag      300
gctagtgaac acagaaagaa gaagtggaca ctgagcttga agaacctgaa gcctgaagac      360
agtggcaagt acacgtgccg tgtatctaac aaggccggtg ccatcaacgc cacctacaaa      420
gtggatgtaa tcc                                         433
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<210> 129

<211> 144

<212> PRT

<213> Mouse

<400> 129

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Met Thr Arg Ser Pro Ala Leu Leu Leu Leu Leu Leu Gly Ala Leu Pro
 1              5              10              15
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Ser	Ala	Glu	Ala	Ala	Arg	Asp	Asp	Ile	Ser	Pro	Gly	Lys	Glu	Ser	Pro
			20					25					30		
Gly	Pro	Gly	Gly	Ser	Ser	Gly	Gly	Gln	Glu	Asp	Pro	Ala	Ser	Gln	Gln
		35					40					45			
Trp	Ala	Arg	Pro	Arg	Phe	Thr	Gln	Pro	Ser	Lys	Met	Arg	Arg	Arg	Val
	50					55					60				
Ile	Ala	Arg	Pro	Val	Gly	Ser	Ser	Val	Arg	Leu	Lys	Cys	Val	Ala	Ser
65					70					75					80
Gly	His	Pro	Arg	Pro	Asp	Ile	Met	Trp	Met	Lys	Asp	Asp	Gln	Thr	Leu
				85					90					95	
Thr	His	Leu	Glu	Ala	Ser	Glu	His	Arg	Lys	Lys	Lys	Trp	Thr	Leu	Ser
			100					105					110		
Leu	Lys	Asn	Leu	Lys	Pro	Glu	Asp	Ser	Gly	Lys	Tyr	Thr	Cys	Arg	Val
		115					120					125			
Ser	Asn	Lys	Ala	Gly	Ala	Ile	Asn	Ala	Thr	Tyr	Lys	Val	Asp	Val	Ile
	130					135					140				

<210> 130
 <211> 502
 <212> DNA
 <213> Mouse

<400> 130	
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gcgcgagatg atattagtcc aggggaaggag agccctgggc caggtgggtc ttcggggggc	120
caggaggacc cagccagcca gcagtgggag cggactcggt ccaagcctgt gctcacaggg	180
acacaccctg tgaacacaac ggtggacttc ggtgggacaa cgtccttcca gtgcaagggtg	240
cgcagtgacg tgaagcctgt gatccagtgg ctgaagcggg tggagtacgg ctccgaggga	300
cgccacaact ccaccattga tgtgggtggc cagaagtttg tgggtgttgc cacgggtgat	360
gtgtgggtcac ggctgatgg ctctacctc aacaagctgc tcatctctcg ggcccgccag	420
gatgatgctg gcatgtacat ctgcctaggt gcaaatacca tgggctacag tttccgtagc	480
gccttctca ctgtattacc ag	502

<210> 131
 <211> 167
 <212> PRT
 <213> Mouse

<400> 131	
Met Thr Arg Ser Pro Ala Leu Leu Leu Leu Leu Gly Ala Leu Pro	
1	15
Ser Ala Glu Ala Ala Arg Asp Asp Ile Ser Pro Gly Lys Glu Ser Pro	
	20 25 30
Gly Pro Gly Gly Ser Ser Gly Gly Gln Glu Asp Pro Ala Ser Gln Gln	
	35 40 45
Trp Glu Arg Thr Arg Ser Lys Pro Val Leu Thr Gly Thr His Pro Val	
	50 55 60
Asn Thr Thr Val Asp Phe Gly Gly Thr Thr Ser Phe Gln Cys Lys Val	
65	70 75 80
Arg Ser Asp Val Lys Pro Val Ile Gln Trp Leu Lys Arg Val Glu Tyr	
	85 90 95
Gly Ser Glu Gly Arg His Asn Ser Thr Ile Asp Val Gly Gly Gln Lys	
	100 105 110
Phe Val Val Leu Pro Thr Gly Asp Val Trp Ser Arg Pro Asp Gly Ser	
	115 120 125
Tyr Leu Asn Lys Leu Leu Ile Ser Arg Ala Arg Gln Asp Asp Ala Gly	
	130 135 140

Met Tyr Ile Cys Leu Gly Ala Asn Thr Met Gly Tyr Ser Phe Arg Ser
 145 150 155 160
 Ala Phe Leu Thr Val Leu Pro
 165

<210> 132
 <211> 706
 <212> DNA
 <213> Mouse

<400> 132
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 gcgcgagcac ggccctcgctt cacacagccc tccaagatga ggcgccgagt gattgcacgg 120
 cctgtgggta gctctgtgcg gctcaagtgt gtggccagtg ggcacccacg gccagacatc 180
 atgtggatga aggatgacca gaccttgacg catctagagg ctagtgaaca cagaaagaag 240
 aagtggacac tgagcttgaa gaacctgaag cctgaagaca gtggcaagta cacgtgccgt 300
 gtatctaaca aggccggtgc catcaacgcc acctacaaag tggatgtaat ccagcggact 360
 cgttccaagc ctgtgctcac agggacacac cctgtgaaca caacggtgga cttcggtggg 420
 acaacgtcct tccagtgcaa ggtgcgcagt gacgtgaagc ctgtgatcca gtggctgaag 480

 cgggtggagt acggctccga gggacgccac aactccacca ttgatgtggg tggccagaag 540
 tttgtggtgt tgcccacggg tgatgtgtgg tcacggcctg atggctccta cctcaacaag 600
 ctgctcatct ctcgggcccg ccaggatgat gctggcatgt acatctgcct aggtgcaaat 660
 accatgggct acagtttccg tagcgccttc ctcactgtat taccag 706

<210> 133
 <211> 235
 <212> PRT
 <213> Mouse

<400> 133
 Met Thr Arg Ser Pro Ala Leu Leu Leu Leu Leu Leu Gly Ala Leu Pro
 1 5 10 15
 Ser Ala Glu Ala Ala Arg Ala Arg Pro Arg Phe Thr Gln Pro Ser Lys
 20 25 30
 Met Arg Arg Arg Val Ile Ala Arg Pro Val Gly Ser Ser Val Arg Leu
 35 40 45
 Lys Cys Val Ala Ser Gly His Pro Arg Pro Asp Ile Met Trp Met Lys
 50 55 60
 Asp Asp Gln Thr Leu Thr His Leu Glu Ala Ser Glu His Arg Lys Lys
 65 70 75 80
 Lys Trp Thr Leu Ser Leu Lys Asn Leu Lys Pro Glu Asp Ser Gly Lys
 85 90 95
 Tyr Thr Cys Arg Val Ser Asn Lys Ala Gly Ala Ile Asn Ala Thr Tyr
 100 105 110
 Lys Val Asp Val Ile Gln Arg Thr Arg Ser Lys Pro Val Leu Thr Gly
 115 120 125
 Thr His Pro Val Asn Thr Thr Val Asp Phe Gly Gly Thr Thr Ser Phe
 130 135 140
 Gln Cys Lys Val Arg Ser Asp Val Lys Pro Val Ile Gln Trp Leu Lys
 145 150 155 160
 Arg Val Glu Tyr Gly Ser Glu Gly Arg His Asn Ser Thr Ile Asp Val
 165 170 175
 Gly Gly Gln Lys Phe Val Val Leu Pro Thr Gly Asp Val Trp Ser Arg
 180 185 190
 Pro Asp Gly Ser Tyr Leu Asn Lys Leu Leu Ile Ser Arg Ala Arg Gln
 195 200 205

Asp Asp Ala Gly Met Tyr Ile Cys Leu Gly Ala Asn Thr Met Gly Tyr
 210 215 220
 Ser Phe Arg Ser Ala Phe Leu Thr Val Leu Pro
 225 230 235

<210> 134
 <211> 340
 <212> DNA
 <213> Mouse

<400> 134
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 gcgcgaggac ccccaagaat ggcagacaaa gtggtccac ggcaggtggc ccgcctgggc 120
 cgactgtgc ggctacagt cccagtggag ggggaccac caccgttgac catgtggacc 180
 aaagatggcc gcacaatcca cagtggctgg agccgcttcc gtgtgctgcc ccagggctcg 240
 aaggtgaagg aggtggaggc cgaggatgcc ggtgtttatg tgtgcaaggc caccaatggc 300
 tttggcagcc tcagcgtcaa ctacactctc atcatcatgg 340

<210> 135
 <211> 113
 <212> PRT
 <213> Mouse

<400> 135
 Met Thr Arg Ser Pro Ala Leu Leu Leu Leu Leu Leu Gly Ala Leu Pro
 1 5 10 15
 Ser Ala Glu Ala Ala Arg Gly Pro Pro Arg Met Ala Asp Lys Val Val
 20 25 30
 Pro Arg Gln Val Ala Arg Leu Gly Arg Thr Val Arg Leu Gln Cys Pro
 35 40 45
 Val Glu Gly Asp Pro Pro Pro Leu Thr Met Trp Thr Lys Asp Gly Arg
 50 55 60
 Thr Ile His Ser Gly Trp Ser Arg Phe Arg Val Leu Pro Gln Gly Leu
 65 70 75 80
 Lys Val Lys Glu Val Glu Ala Glu Asp Ala Gly Val Tyr Val Cys Lys
 85 90 95
 Ala Thr Asn Gly Phe Gly Ser Leu Ser Val Asn Tyr Thr Leu Ile Ile
 100 105 110
 Met

<210> 136
 <211> 148
 <212> DNA
 <213> Mouse

<400> 136
 atgacgcgga gccccgcgct gctgctgctg ctattggggg ccctcccgtc ggctgaggcg 60
 gcgcgagatg atattagtcc aggggaaggag agccctgggc caggtgggtc ttcggggggc 120
 caggaggacc cagccagcca gcagtggg 148

<210> 137
 <211> 49
 <212> PRT
 <213> Mouse

<400> 137

Met Thr Arg Ser Pro Ala Leu Leu Leu Leu Leu Leu Gly Ala Leu Pro
 1 5 10 15
 Ser Ala Glu Ala Ala Arg Asp Asp Ile Ser Pro Gly Lys Glu Ser Pro
 20 25 30
 Gly Pro Gly Gly Ser Ser Gly Gly Gln Glu Asp Pro Ala Ser Gln Gln
 35 40 45
 Trp

<210> 138
 <211> 352
 <212> DNA
 <213> Mouse

<400> 138
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 gcgcgagcac ggctcgcgtt cacacagccc tccaagatga ggcgccgagt gattgcacgg 120
 cctgtgggta gctctgtgcg gctcaagtgt gtggccagtg ggcacccacg gccagacatc 180
 atgtggatga aggatgacca gaccttgacg catctagagg ctagtgaaca cagaaagaag 240
 aagtggacac tgagcttgaa gaacctgaag cctgaagaca gtggcaagta cacgtgccgt 300
 gtatctaaca aggccggtgc catcaacgcc acctacaaa tggtatgtaat cc 352

<210> 139
 <211> 117
 <212> PRT
 <213> Mouse

<400> 139

Met Thr Arg Ser Pro Ala Leu Leu Leu Leu Leu Leu Gly Ala Leu Pro
 1 5 10 15
 Ser Ala Glu Ala Ala Arg Ala Arg Pro Arg Phe Thr Gln Pro Ser Lys
 20 25 30
 Met Arg Arg Arg Val Ile Ala Arg Pro Val Gly Ser Ser Val Arg Leu
 35 40 45
 Lys Cys Val Ala Ser Gly His Pro Arg Pro Asp Ile Met Trp Met Lys
 50 55 60
 Asp Asp Gln Thr Leu Thr His Leu Glu Ala Ser Glu His Arg Lys Lys
 65 70 75 80
 Lys Trp Thr Leu Ser Leu Lys Asn Leu Lys Pro Glu Asp Ser Gly Lys
 85 90 95
 Tyr Thr Cys Arg Val Ser Asn Lys Ala Gly Ala Ile Asn Ala Thr Tyr
 100 105 110
 Lys Val Asp Val Ile
 115

<210> 140
 <211> 421
 <212> DNA
 <213> Mouse

<400> 140
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 gcgcgagagc ggactcgttc caagcctgtg ctcacaggga cacaccctgt gaacacaacg 120
 gtggacttcg gtgggacaac gtccttcag tgcaagggtg gcagtgcgt gaagcctgtg 180
 atccagtggc tgaagcgggt ggagtacggc tccgaggac gccacaactc caccattgat 240
 gtgggtggcc agaagtttgt ggtgttgccc acgggtgatg tgtggtcacg gcctgatggc 300

tcctacctca acaagctgct catctctcgg gcccgccagg atgatgctgg catgtacatc 360
 tgcctagggtg caaataccat gggctacagt ttccgtagcg ccttctctcac tgtattacca 420
 g 421

<210> 141
 <211> 140
 <212> PRT
 <213> Mouse

<400> 141
 Met Thr Arg Ser Pro Ala Leu Leu Leu Leu Leu Leu Gly Ala Leu Pro
 1 5 10 15
 Ser Ala Glu Ala Ala Arg Glu Arg Thr Arg Ser Lys Pro Val Leu Thr
 20 25 30
 Gly Thr His Pro Val Asn Thr Thr Val Asp Phe Gly Gly Thr Thr Ser
 35 40 45
 Phe Gln Cys Lys Val Arg Ser Asp Val Lys Pro Val Ile Gln Trp Leu
 50 55 60
 Lys Arg Val Glu Tyr Gly Ser Glu Gly Arg His Asn Ser Thr Ile Asp
 65 70 75 80
 Val Gly Gly Gln Lys Phe Val Val Leu Pro Thr Gly Asp Val Trp Ser
 85 90 95
 Arg Pro Asp Gly Ser Tyr Leu Asn Lys Leu Leu Ile Ser Arg Ala Arg
 100 105 110
 Gln Asp Asp Ala Gly Met Tyr Ile Cys Leu Gly Ala Asn Thr Met Gly
 115 120 125
 Tyr Ser Phe Arg Ser Ala Phe Leu Thr Val Leu Pro
 130 135 140

<210> 142
 <211> 67
 <212> DNA
 <213> Mouse

<400> 142
 atgacgcgga gccccgcgct gctgctgctg ctattggggg ccctcccgtc ggctgaggcg 60
 gcgcgag 67

<210> 143
 <211> 22
 <212> PRT
 <213> Mouse

<400> 143
 Met Thr Arg Ser Pro Ala Leu Leu Leu Leu Leu Leu Gly Ala Leu Pro
 1 5 10 15
 Ser Ala Glu Ala Ala Arg
 20

<210> 144
 <211> 1389
 <212> DNA
 <213> Mouse

<400> 144
 atgacgcgga gccccgcgct gctgctgctg ctattggggg ccctcccgtc ggctgaggcg 60
 gcgcgaggac cccaagaat ggcagacaaa gtgggtccac ggcaggtggc ccgcctgggc 120


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cgactgtgc ggctacagtg cccagtggag ggggacccac caccgttgac catgtggacc 180
aaagatggcc gcacaatcca cagtggctgg agccgcttcc gtgtgctgcc ccagggctctg 240
aaggtgaagg aggtggaggc cgaggatgcc ggtgtttatg tgtgcaaggc caccaatggc 300
tttggcagcc tcagcgtcaa ctacactctc atcatgtgga tgaaggatga ccagaccttg 360
acgcacttag aggctagtga acacagaaag aagaagtgga cactgagctt gaagaacctg 420
aagcctgaag acagtggcaa gtacacgtgc cgtgtatcta acaaggccgg tgccatcaac 480
gccacctaca aagtggatgt aatccagcgg actcgttcca agcctgtgct cacagggaca 540
caccctgtga acacaacggc ggacttcggt gggacaacgt ccttccagtg caaggtgcgc 600
agtgcagtga agcctgtgat ccagtggctg aagcgggtgg agtacggctc cgagggacgc 660
cacaactcca ccattgatgt gggtgccag aagtttgtgg tgttgccac gggatgtg 720
tggtcacggc ctgatggctc ctacctcaac aagctgctca tctctcgggc ccgccaggat 780
gatgctggca tgtacacctg cctaggtgca aataccatgg gctacagttt ccgtagcgcc 840
ttcctcactg tattaccaga ccccaaacct ccagggcctc ctatggcttc ttcactgctc 900
tccacaagcc tgccatggcc tgtggtgatc ggcattccag ctggtgctgt cttcactcta 960
ggcactgtgc tgctctggct ttgccagacc aagaagaagc catgtgcccc agcatctaca 1020
cttctgtgct ctgggcatcg tccccaggg acatcccgag aacgcagtgg tgacaaggac 1080
ctgccctcat tggctgtggg catatgtgag gagcatggat ccgccatggc cccccagcac 1140
atcctggcct ctggtcctaac tgctggcccc aagctgtacc ccaagctata cacagatgtg 1200
cacacacaca cacatacaca cacctgcact cacacgctct catgtggagg gcaaggttca 1260
tcaacaccag catgtccact atcagtgcta aatacagcga atctccaagc actgtgtcct 1320
gaggtaggca tatggggggc aaggcaacag gttggggagaa ttgagaacaa tggaggaaga 1380
gtatcttag 1389

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<210> 145
 <211> 462
 <212> PRT
 <213> Mouse

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<400> 145
Met Thr Arg Ser Pro Ala Leu Leu Leu Leu Leu Leu Gly Ala Leu Pro
 1          5          10          15
Ser Ala Glu Ala Ala Arg Gly Pro Pro Arg Met Ala Asp Lys Val Val
 20          25          30
Pro Arg Gln Val Ala Arg Leu Gly Arg Thr Val Arg Leu Gln Cys Pro
 35          40          45
Val Glu Gly Asp Pro Pro Pro Leu Thr Met Trp Thr Lys Asp Gly Arg
 50          55          60
Thr Ile His Ser Gly Trp Ser Arg Phe Arg Val Leu Pro Gln Gly Leu
 65          70          75          80
Lys Val Lys Glu Val Glu Ala Glu Asp Ala Gly Val Tyr Val Cys Lys
 85          90          95
Ala Thr Asn Gly Phe Gly Ser Leu Ser Val Asn Tyr Thr Leu Ile Met
 100          105          110
Trp Met Lys Asp Asp Gln Thr Leu Thr His Leu Glu Ala Ser Glu His
 115          120          125
Arg Lys Lys Lys Trp Thr Leu Ser Leu Lys Asn Leu Lys Pro Glu Asp
 130          135          140
Ser Gly Lys Tyr Thr Cys Arg Val Ser Asn Lys Ala Gly Ala Ile Asn
 145          150          155          160
Ala Thr Tyr Lys Val Asp Val Ile Gln Arg Thr Arg Ser Lys Pro Val
 165          170          175
Leu Thr Gly Thr His Pro Val Asn Thr Thr Val Asp Phe Gly Gly Thr
 180          185          190
Thr Ser Phe Gln Cys Lys Val Arg Ser Asp Val Lys Pro Val Ile Gln
 195          200          205
Trp Leu Lys Arg Val Glu Tyr Gly Ser Glu Gly Arg His Asn Ser Thr
 210          215          220

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Ile Asp Val Gly Gly Gln Lys Phe Val Val Leu Pro Thr Gly Asp Val
 225 230 235 240
 Trp Ser Arg Pro Asp Gly Ser Tyr Leu Asn Lys Leu Leu Ile Ser Arg
 245 250 255
 Ala Arg Gln Asp Asp Ala Gly Met Tyr Ile Cys Leu Gly Ala Asn Thr
 260 265 270
 Met Gly Tyr Ser Phe Arg Ser Ala Phe Leu Thr Val Leu Pro Asp Pro
 275 280 285
 Lys Pro Pro Gly Pro Pro Met Ala Ser Ser Ser Ser Thr Ser Leu
 290 295 300
 Pro Trp Pro Val Val Ile Gly Ile Pro Ala Gly Ala Val Phe Ile Leu
 305 310 315 320
 Gly Thr Val Leu Leu Trp Leu Cys Gln Thr Lys Lys Lys Pro Cys Ala
 325 330 335
 Pro Ala Ser Thr Leu Pro Val Pro Gly His Arg Pro Pro Gly Thr Ser
 340 345 350
 Arg Glu Arg Ser Gly Asp Lys Asp Leu Pro Ser Leu Ala Val Gly Ile
 355 360 365
 Cys Glu Glu His Gly Ser Ala Met Ala Pro Gln His Ile Leu Ala Ser
 370 375 380
 Gly Ser Thr Ala Gly Pro Lys Leu Tyr Pro Lys Leu Tyr Thr Asp Val
 385 390 395 400
 His Thr His Thr His Thr His Thr Cys Thr His Thr Leu Ser Cys Gly
 405 410 415
 Gly Gln Gly Ser Ser Thr Pro Ala Cys Pro Leu Ser Val Leu Asn Thr
 420 425 430
 Ala Asn Leu Gln Ala Leu Cys Pro Glu Val Gly Ile Trp Gly Pro Arg
 435 440 445
 Gln Gln Val Gly Arg Ile Glu Asn Asn Gly Gly Arg Val Ser
 450 455 460